```
9b_gss9; AO616191

9b_est28: ALJ037695

9b_gss20: AZ36344

9b_gss21: AZ416308

9b_gss21: AZ711250

9b_gss10: AQ771250

9b_gss15: AZ078264

9b_est66: BE033430

9b_gss23: BH7827

9b_gss23: BH7827
              gb_est72:BE532096
gb_gss1:AQ026784
gb_gss1:AZ020787
gb_est66:BE03679
gb_est70:BE396460
gb_est77:BE396109
gb_gss1:AZ209601
gb_est75:BE782836
gb_est75:BE782836
gb_est75:BE791044
gb_est78:BE366571
                                                                                                                                                                                                                                                          gh_est75:BE734359
gh_est79:BE037592
gh_est68:BE250598
gh_est77:BE872484
gh_est77:BE872484
gh_est78:BE78035
gh_est78:BE78035
gh_est78:BE96268
gh_est78:BE96268
gh_est78:BE96268
gh_est78:BE96268
gh_est78:BE96268
gh_est78:BE963687
gh_est78:BE963687
gh_est77:BE838502
gh_est77:BE838503
gh_est77:BE8375630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM of: US-09-510-332-1 to: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database sequences: 7991742
Database length: -79123438
Search time (sec): 491.860000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Date: Mar 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query length: 299
Database: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block:
Query: US-09-510-332-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -MODEL-frame+p2n.model -DEV-xlp
-Q-/cgn2_1/USPTO_spool/US9510332/runat_06032001_093637_13621/app_query.fasta_1.359
-Q-/cgn2_1/USPTO_spool/US9510332/runat_06032001_093637_13621/app_query.fasta_1.359
-DB-EST -QEMT=fastap -SUFFIX-ras -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=20 -THR_SCORE-pct -THR_MAX=100 -THR_MIN=0
-ALIGN=15 -MODE-LOCAL -OUTEMT=p5s -NORM-ext -MIXLEN=0
-MAXLEN=2000000000 -USER=US09510332_@CGN1_1_2364 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d orig
1165.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PX
150.50

157.50

157.50

148.00

147.50

141.50

135.50

135.50

135.50

134.00

135.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

132.50

133.00

134.00

134.00

134.00

136.50

137.50

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

128.00

127.50

127.50

127.50

127.50

127.50
  2830 ore
2073.39
2073.39
851.56
9851.56
9851.68
304.39
2083.83
2267.60
2242.45
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
2230.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 out_format : pfs
  0.0027
0.0027
0.0022
0.0017
0.0034
0.0035
0.0039
0.0019
0.0022
0.0027
0.0037
0.0039
0.0039
0.0039
0.0034
0.0034
0.0034
0.0034
0.0034
                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0002
0.0007
0.0008
0.0009
0.0006
0.0001
0.0011
0.0016
0.0017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.5e-07
6.7e-06
2.4e-05
7.9e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.0e-38
5.0e-33
5.3e-11
1.8e-09
5.3e-08
6.1e-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EScore Len
                                                                                                                                                                                                                                                                                                                                           1176
466
1542
1502
1652
1689
993
1378
1378
1324
1324
1625
1420
1649
1651
1291
    1111
1395
817
875
925
1050
1329
1678
838
1678
1142
1142
1143
1143
1143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ._
                   AQ316999 CITBI E1-2530B8.TF CIT AQ3186999 CITBI E1-2530B7.TF CIT AQ3186999 CITBI E1-2530B7.TF CIT AQ277039 CITBI E1-2516A7.TF CIT AQ277039 CITBI E1-2516A7.TF CIT AQ4155B1 zu05ed4.sl Scares_test AQ616191 HS_5148_A2_F05_SP6E RF AQ4155B1 zu05ed4.sl Scares_test AQ616191 HS_5148_B2_F05_SP6E RF AQ4165B1 NM019504R MOUSE 10kb AQ4165B1 M019504R MOUSE 10kb AQ718264 RPCI-33-399P19.TV RPCI AZ393439 MEDIFOR ME MESEMBLY94 BBC307592 601461160F1 NIH_MGC_B BE303430 MEDIFOR ME MESEMBLY94 BBC307592 601447162F1 NIH_MGC_B BE30598 60093379F1 NIH_MGC_B BE30504 601655058R1 NIH_MGC_B BE78135 601469204F1 NIH_MGC_B BE78135 601469204F1 NIH_MGC_B BE78135 601457540F1 NIH_MGC_B BE78135 601457540F1 NIH_MGC_B BE78135 601467528F1 NIH_MGC_B BE338364 601655058R1 NIH_MGC_B BE338502 601287177F1 NIH_MGC_B BE338502 601487528F1 NIH_MGC_B BE33966 601285518F1 NIH_MGC_B BE33966 601285518F1 NIH_MGC_B BE336509 RPD6801 MP MESEMBLY941 BE784050 SPD6811 MP MESEMBLY941 BE784050 SPD6811 MP MESEMBLY941 BE784056 STD NIH_MGC_B BE33660 NED6801 MP MESEMBLY941 BE784056 STD NIH_MGC_B BE33660 NED6801 MP MESEMBLY941 BE784050 SPD6811 MIH_MGC_B BE33660 NED6801 MP MESEMBLY941 BE784060 SPD6811 MP MESEMBLY941 BE784060 SPD6811 MP MESEMBLY941 BE784060 SPD6811 MP MESEMBLY941 BE784060 SPD6811 MP MESEMBLY941 BE784060 MD08611 MP MESEMBLY941 BE7865 STD NIH_MGC_B BE65571 MO14660_SFGE STD NIH_MGC_B BE66571 MO14660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Documentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                     Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                      90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176
```

```
gb_est68:BE214090
gb_gss17:AZ196311
gb_est78:BE960997
gb_est66:BE040951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_gss4:AQ308694
                                                                                                                                                                                                                                                                                 alignment_scores:
Quality: 1165.00
Ratio: 5.155
Percent Similarity: 100.000
                                                                                                                                                                                                                                  alignment_block:
US-09-510-332-1 x AQ308694
sequence.
AQ308694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ308694 742 bp DNA
CITBI-E1-2530B8.TF CITBI-E1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 742)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ308694.1 GI:4040728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Venter,J.C.\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clones are availabe from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hbe@tigr.org
                                                                                                                                                                                                   AQ308694 from: 1 to: 742
                                                                                                                                                                                                                                                                                                                                                                                                      ø
                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
175 c 144 g 247 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2530B8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CITBI-E1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        127.50
127.00
127.00
127.00
127.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1215.36
220.73
218.89
217.34
                                                                                                                                                                                                                                                                                      Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0055
0.0028
0.0035
0.0043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                     226
0
100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1640 | BE214090 HV_CEb0002D06f Hor 904 | AZ196311 SP_1031_B2_C06_T7A 1075 | BE960997 601648553F1 NIH_MG 1245 | BE040951 OF15A01 OF OTYZA S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 22-DEC-1998 genomic clone 2530B8,
          151
                                         123
                                                                       101
                                                                                                          107
                                                                                                                                         51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
```

```
JOURNAL COMMENT
                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS AQ316999
                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                    seq_name: gb_gss4:AQ316999
                                                                                                                                                                                                                                               DEFINITION
                                                                                                              TITLE
                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                             290
                                                                                                                                                                                                                                                                                                         652
                                                                                                                                                                                                                                                                                                                                                  602
                                                                                                                                                                                                                                                                                                                                                                                         552
                                                                                                                                                                                                                                                                                                                                                                                                           257
                                                                                                                                                                                                                                                                                                                                                                    274
                                                                                                                                                                                                                                                                                                                                                                                                                              502
                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157
                                                                                                                                                                                                                                                                                                                                                                                                                         sPheLeuLeuH1sSerLysCysCysGln 299
                                                                                                                                                                                                                                                                                                                                          InMetargAsnThrValAlaGlySerArgValProGlyArgGlyAlaPro
                                                                                                                                                                                                                                                                                                      GTTCCTCCACAGTAAGTGCTGTCAG
                                                                                                                                                                                                                                                                                                                                                                                  TCATCTTTCTGTTCTTCATCCTTGTGATTGGTATATACCCTTCTGGACAC
                                                                                                                                                                                                                                                                                                                                                                                              heIlePheLeuPhePheIleLeuVallleGlyIleTyrProSerGlyH1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Map Building
Unpublished (1998)
Unpublished (1998)
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
 end
    Email: hbe@tigr.org
Clones are availabe from Research Genetics (info@resgen.com).
                           9712 Medical Center Dr.,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                      Berry, K., o
                                                                                                                                                                                                                         AQ316999
                                                                                                                                                                                                                                            AQ316999 650 k
CITBI-E1-2530B7.TF
                                                                                                           Use of a random human BAC
                                                                                                                           Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S.,
Berry,K., Granger,D., Suh,E., Wible,C., Shiz
                                                                                                                                                   Mammalia; Eutheria;
1 (bases 1 to 650)
                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                               AQ316999.1 GI:4040265
search page:
                                                                                                                                                                                                                                       bp DNA GSS
F CITBI-El Homo sapiens genomic
                                                                                                           End
                                                                                                                                                                                                                                                                                                       679
                                                                                                           Sequence
                                                                                                          Database
                                                                             Mark
                                                                                                                           s,S., Linher,K., Golden,K.
Shizuya,H., Simon,M. and
                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                              257
                                                                                                                                                                                                                                                                                                                                                                                   601
                                                                                                                                                                                                                                                                                                                                                                                                       273
                                                                                                                                                                                                                                                                                                                                                                                                                           551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           157
                                                                                                                                                                                                                                         clone 2530B7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140
                                                                                                       Sequence-Ready
                                                                                                                                                                                                                                         DNA
```

```
BASE C
                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-510-332-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 1106.00
Ratio: 5.120
Percent Similarity: 100.000
            257
                            502
                                                             452
                                                                                              402
                                                                             224
                                                                                                                              352
                                                                                                                                                           207
                                                                                                                                               190
                                                                                                                                                                                                                                                                                               252
                                                                                                                                                                                                                 157
                                                                                                                                                                                                                                 202
                                                                                                                                                                                                                                                 140
                                                                                                                                                                                                                                                                  152
                                                                                                                                                                                                                                                                       124 LysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSerMetIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNT
                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                         74 GluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGl
                                                                                                                                                                                                                                                                                                                                                                heIlePheLeuPhePheIleLeuValIleGlyIleTyrProSerGlyHis
                        AAATGAGAAACACAGTGGCCGGCAGCAGGGTTCCTGGCAGGGGTGCACCC
                                                                                                                          AAGCTGGTCCCATGGATGATCCTGGGGTCTCTGCTATATGTATCTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149
                                                                                                                                                                                                                                                                                                                                                                                                                    ×
                                                                                                                                                                                                                                                                                                                                                                                                                    AQ316999
                                                                                                                                                                                                                                                                                                                                                                                                   AQ316999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /Sex="male"
/Cell_type="sperm"
/note="Vector: pBeloBAC11;
/note="Vector: pBeloBAC11;
CalTech Human BAC Library C
CalTech Human BAC Library C
224 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2530B7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CITBI-E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                  ţo:
                                                                                                                                                                                                                                                                                                                                                                                                   650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Site_1: ECORI; Site_2: ECORI; t
                                                                                                                                                                                                                                                                                                                                                                                                                                           100.000
                         551
                                                                          240
        273
                                         257
                                                          501
                                                                                           451
                                                                                                                             401
                                                                                                                                                                                                                                                                              140
                                                                                                            223
                                                                                                                                            207
                                                                                                                                                             351
                                                                                                                                                                             190
                                                                                                                                                                                             301
                                                                                                                                                                                                             173
                                                                                                                                                                                                                              251
                                                                                                                                                                                                                                              157
                                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                                                                                                                                                                107
                                                                                                                                                                                                                                                              201
                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                 51
                                                                                                                                                                                                                                                                                                                                                                                  90
```

TCATCTTTCTGTTCATCCTTGTGATTGGTATATACCCTTCTGGACAC 601

```
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_gss4:AQ277039
                                                                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /ERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                alignment_block:
                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                            US-09-510-332-1 x AQ277039
                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                              140
                                                                                                                                                       124 LysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSerMetIl 140
                     157
                                                         53 ACGTGTTCTCCATAGCAAATATGCAGGGTTTATGGTCCCATACTTCCTAA 102
                                                                                                                                  3 AAGCTGGTCCCATGGATGATCCTGGGGTCTCTGCTATATGTATCTATGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerLeuIleLeuIleLeuGlyAsnProLysLeuLysGlnAsnAlaLys 289
rgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThrLeuAla 173
                                                                          eCysValPheHisSerLysTyrAlaGlyPheMetValProTyrPheLeuA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ277039 310 t
CITBI-E1-2516A7.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 310)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Mark Adams
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_GSSs: CITBI-E1-2516A7.TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.
Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ277039.1
                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                           to: AQ277039
                                                                                                                                                                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI; CalTech Human BAC Library D"
77 c 69 g 88 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2516A7"
                                                                                                                                                                                                                                                                                                   455.00
4.643
96.078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="sperm"
/note="Vector: pBei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CITBI-E1"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:3903235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp DNA
F CITBI-E1
                                                                                                                                                                                                             from: 1 to: 310
                                                                                                                                                                                                                                                                                            Length: 102
Gaps: 0
Percent Identity: 90.196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSS 22-NOV-1998 sapiens genomic clone 2516A7, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MD 20850, USA
                                                                                                                                      52
```

```
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name:
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 IleGlnIlePheSerPheValAlaGluPheSerValProLeuLeuIlePh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103 GGAAATTNTTCTCCCAAAATGCCACAATTCAAAAAGAAGATACACTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 IleSer 225
                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lnMetArgAsnThrValAlaGlySerArgValProGlyArgGlyAlaPro 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eLeuPheAlaValLeuLeuLeuIlePheSerLeuGlyArgHisThrArgG
|||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAATGAGAAACACAGCGGCCGGCAGCAGGGTTCCTGGCAGGGGTGCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCAGC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est7:AA416581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. WashU-Merck EST project 1997
unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA416581 463 bp mRNA EST 16-OCT-1997
Zu05e04.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 463)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA416581.1 GI:2077515
                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -41m13 fwd. Er from Amersham High quality sequence stop: 413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA416581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                       Email: est@watson.wustl.edu
                 140
            /organism="Homo sapiens"
/db_xref="GDB:5927764"
                                                                                                                                                                                                                                    /clone_lib="Soares_testis_NHT"
                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/clone="IMAGE:730974"
                                                                                                                                                                                                    'lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomí;
```

alignment_scores: Quality:

406.00

Length:

```
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AQ616191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 4.892
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-510-332-1 x AA416581/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 euLeuSerCysLeuAlaValSerArgIlePheLeuGlnLeuPheIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTCTTTCTTGTCTGGCAGTTTCTAGAATTTTTCTGCAGTTGTTCATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAATTGTGCAATTCTCTTATTTATAAATGAATTGGAACTTTGGCTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_gss9:AQ616191
                                                                                                                                                                                           Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Clones availability, please contact Pleter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 bp DNA GSS 15-JUN-1999
HS_5148_A2_F05_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=724 Col=10 Row=K, DNA sequence.
A0616191
                                                                                                                             http://www.htsc.washington.edu
Plate: 724 row: K column: 10
Seq primer: SP6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 498)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
                                                                                                                                                                                                                                                                                                               401 Queen Anne Avenué North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                High Throughput Sequencing Center University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ616191.1 GI:5077555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to reverse of: AA416581
                                                                                          quality sequence stop: 498 Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=724 Col=10 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 0
Percent Identity: 97.590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from:
                                                                                                                                                                                                                                                                                                                                                                                                    Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                              KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                 ACCESSION
VERSION
                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                  472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375
                                                                                                                                                                                                                                                                                                                                                                                                                                  145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
```

```
seq_documentation_block:
LOCUS AL037695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est28:AL037695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-510-332-1 x AQ616191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422 GCTTCTGGGAAGCGGTCTGGCCTCTGTGAGCATTGCATCTGTGTGTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 roLeuPheIleTrpLeuLysMetArgIleSer.LysLeuValProTrpMe 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 CATAGCGATGTCTACAATTGGTCTGCAGATGGTGGTAATGGTACAAAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 GAATTGATCAAACATAGAAAGCTAATGCCAATTCAAATCCTCTTAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50 sLeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTCTCTGTGTTCTTTCCACTCCTTTACGTCAAAATAATCTATGGTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerLysTyrAla 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tIleLeuGlySer...LeuLeuTyrValSerMetIleCysVal.PheHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGTTTTCTTTGGTGAAATTCAGGA...TCCAAAGGTAATACCTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aThrTrpLeuGlyValPheTyrCysAlaLysValAlaSerValArgHisP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAATGACGTTCCTTTGGATGTTTTTTAACTCTATCAGCCTATGGGTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAl 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  allleValllephephe......IleGluPheIleMetCysSer 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAGATTACGCC
                                                               Blum,H., Bauersachs,S., Mewes,H.W.,
EST (Blum, et al.)
Unpublished (1999)
On Jul 7, 1999 this sequence version
                                                                                                                                                                                                                                                                                                                                                         AL037695 554 bp mRNA EST DKFZp56400672_r1 564 (synonym: hfbr2) Homo DKFZp56400672 5', mRNA sequence.
Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert
                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                   AL037695.3 GI:5928268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                 (bases 1 to 554)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; wale blood DNA was isolated from one randomly chosen de and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites"

104 c 112 g 155 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197.00
2.402
67.213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from:
                                                                                                                                                                                                    Chordata;
Primates;
                                                                                     sequence version replaced gi:5866546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                         Gassenhuber,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122
5
39.344
                                                                                                                                                                                                                                                                                                                                                                                   sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 224
                                                                                                                                                         and Wiemann, S
                                                                                                                                                                                                                                                                                                                                                                                                         29-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            donor
```

sequence of

```
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
seq_documentation_block:
LOCUS AZ396344
                                                           seq_name: gb_gss20:AZ396344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AL037695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-510-332-1 x AL037695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                    305
                                                                                                                                                     138
                                                                                                                                                                                                 355
                                                                                                                                                                                                                                                                                                         205 TTATATAGTTTAGAAGTAAGAATTGTTCCTTCTAATGTCTCGGCAATAAT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 TCTCCTCAACTGACCAAATTGTCACTGCTCTGGCATTCTCCAGAATTGGT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58 LeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheIleGl 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 etAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePhe 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 nGlyIleIleValValAsnGlyIleAspLeuIleLysHisArgLysM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uphelleMet.CysSerAlaAsnCysAlaIle.....Leu.LeuPhell 88
                                                                                                                                                                                                                                                                                                                                                                                                              eAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysA 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTACTTTGATCATATTACTTACGTATGCAACTGTGTTTAATTCAGCT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTTTATCAATTCTGGTAGTGTTTGCATTTGTTCTTGGAAATGTTGCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCTTCATAGCTCTAGTTAATGTCAATGACTGGGTTAAGACACAAAAGA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAs
                                                                                                                                                                                                                                                                                    TCAAGATTGCCAATTTCTCCAATTTTATTTTTCTCCACCTAAAGAAGAGA
                                                                                                                                                     rMetIleCys 141
                                                                                                                                                                                                 ATTAAGAGTGTTCTTGTGATACTGTTGGGGTCCTTGGTATTT....
                                                                                                                                                                                                                                      IleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSe 138
                                                                                                                                                                                                                                                                                                                                                                            CAATCATTTCAGCATTTGGCTTGCTACGAGCCTCAGCATATTTTATTTGT 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s1 sequence also available.
This clone (DKrZp56400672) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by LMU (Ludwig Maximilians University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Berlin-Charlottenburg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Munich/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="DKFZp56400672"
/clone_lib="564 (synonym: hfbr2)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
/nota="Vector: ablue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183.00
1.887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.290
  710 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaps: 4
Percent Identity: 35.507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GERMANY;
    DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: clone@rzpd.de.
      GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                         354
      03-OCT-2000
```

```
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
alignment_block:
US-09-510-332-1 x AZ396344/rev
                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1M0160C21R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC1M0160C21 R, DNA sequence.
AZ396344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert B.
University of Utah
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dunn, D., Aoyagi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly, Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AZ396344.1 GI:10511416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: 0160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.
Insert Length: 10000 Std
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse
                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mmalia; Eutheria; (bases 1 to 710)
                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308,
                                                                                                                                                                                                                                                                                                                                                                       216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AF129072.1), a copy-number inductible derivative of plasmid R1. The vector was ligated in the complex complex control of the control of the control of plasmid R1. The vector was ligated in the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                        with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll XLIO-Gold (Stratagene) cells and selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         585 5606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="UUGC1M0160C21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory Mouse DNA Resource
                                                                                                              170.50
1.705
62.893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            row: C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Weiss
Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                      Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            column: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PWD42nv; Purified genomic DNA from M.
                                                                                                                  Identity: 26.415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                           Length:
                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
ა
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
```

Align seg 1/1 to reverse of: AZ396344

from:

1 to:

IleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheTh 23

```
SOURCE
ORGANISM
                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AZ416308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_gss21:AZ416308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 TCACACCTTTCCACTCCATGTAGCAAGCTGGGTCTCCAGGAGATTTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 gHis.....ProLeuPheIle.....TrpLeuLysMetArgIleSerL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 TTCCTGCAG......GGCCTTCTGCTTTTGGATGCTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 ACCAAGCCATCCTCACTCTCTGGATGATTGCAAACCAAGTGAGCCTCTGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 TCAG...CTCGCCTGCTTCCAGCAGGATGAAAGACCCACTGAGCCACAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 TGGGGACTTTTTTGCAGATCTCACTCC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83 AGATGCTTCTAGTTGTTCTTCTTCTCTCCTGCATCTGCACTGCCCCTTGTT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 PheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheIl 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSerMetIle 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSerValAr 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGGCTGCCTCAGTCTCCTCTACTGCTCCAAGATTGTCCGCTTCTC 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ...SerAlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluLeuTrp 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTTGAACAACTGTGACATCGCACTGCTGTGTCTCAGCATCACTCGGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAACGCCTTCATTGTCTTGGTAAATGTTTGGGATGTGGTAAAAAAGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .....CysValPheHisSer 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eGluPheIleMetCys.....
                      Email: ddunn@genetlcs.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0191 row: D column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                 Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 656)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Welss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ416308 656 bp DNA GSS 03-OCT-2000 1M0191D04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0191D04 R, DNA sequence.
AZ416308
                                                                                                                                                                                                                                                              Plasmid inserts
Unpublished (2000)
        High quality sequence stop: 656
                                                                                                                       Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AZ416308.1 GI:10540321
                                                                                                                                                                                    308,
                                                                                                                                                                  USA
                                                                                                                                                                              Biomedical Polymers Research Bldg.,
                                                                                                                                                                                20
                                                                                                                                                                                ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       413
                                                                                                                                                                            2030 E.,
                                                                                                                                                                            SLC,
                                                                                                                                                                            T
seq_documentation_block:
                                  seq_name: gb_gss10:AQ711250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                          337
                                                                                                                 287
                                                                                                                                                                                                                                   387
                                                                                                                                                                                                                                                                          253
                                                                                                                                                                                                                                                                                                              437
                                                                                                                                                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D
```

```
alignment_block:
US-09-510-332-1 x AZ416308/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: AZ416308 from: 1 to: 656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487 AAGTTCATGTGAGAACAATAAAAGTTTTATTGTCTTTTATTATCCTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 sThrargGlnMetargAsnThrValAlaGlySerArgValProGlyArgG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587 ATGATAATGTTAATTGTATGTTTCCTGTTAATCATTTCACTTTGGAGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 LeuIlePheLeuPheAlaValLeuLeuIlePheSerLeuGlyArgH1
                                                                                                                                                         PheSerHisCysMet...IleLysValPheLeuSerSerLeuLysPheH1
                                                          AsnAlaLysLysPheLeuLeuHisSerLysCysCysGln 299
                                                                                                                                                                                                                                                                                                            sIleArgArgPheIlePheLeuPhePheIleLeuValIleGlyIleTyrP
TGCTCTGTAATGATACTGCAACTATTAAAGTGCTGTGAG 249
                                                                                                                        CCGGCTGCCACTCACTTATCCTAATTCTAGCAAACAGTCGGCTGAAGCAG
                                                                                                                                                                                                                                                 AGAAAGCAACTTGTTATTCATGTTTTGGTTTGACAACTGCATTCATCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCGCAGGCAGATGGAATCAAATAAATTAGGATTCAGAGATCTCAACACAG
                                                                                                                                                                                                                                                                                                                                                                          ATATTGCATTCATGGGTATTACCATAAATGTAATTTGTCTGTTAATCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lyAlaProIleSerAlaLeuLeuSerIleLeuSerPheLeuIleLeuTyr 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWDA2 (gil4732114[gb]AF129072.1), a copy-number inducible derivative of plasmid Rl. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/63 (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169.50
2.230
67.257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="UUGC1M0191D04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'clone_lib="Mouse 10kb plasmid UUGCIM library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 113
Gaps: 1
Percent Identity: 38.053
                                                                                                                                                                                      286
                                                                                                                                                                                                                                                                                                               270
                                                                                                                                                                                                                                                                                                                                                                          388
                                                                                                                                                                                                                                                 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438
                                                                                                                        288
                                                                                                                                                                                                                                                                                                                                                                                                                                     253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     538
```

```
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL MEDLINE
                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                  US-09-510-332-1 x AQ711250/rev
                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                             147
                                                                                             488
                                                                                                                                                                                                                                         115 PheIleTrpLeuLysMetArgIleSerLysLeuValProTrpMetIleLe 131
                                                                                                                                      131 uGlySerLeuLeu...TyrValSerMetIleCysValPheHisSerLys. 146
                                                                                                                                                                                         TTTCTTTGGTTGAAATTCAGGATCCCANAGTTAATACCTTGGCT.GTTCT
TACGCTANAAATGTGGAAGAGGATGCCCTCAGA.....
                                           TyralaGlyPheMetValProTyrPheLeuArgLysPhePheSerGlnAs 163
                                                                                             GGGAAGCGTTCTGGCCTCTGTGAGCATGNCATCTGTGTGTCGAGGTAGAT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ711250 538 bp DNA GSS 13-JUL-1999 HS_5349_B2_H04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=925 Col=8 Row=P, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 538)
1 (bases 1 to 538)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Adams,M.D. a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.htsc.washington.edu
plate: 925 row: P column: 8
Seq primer: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scanning the human genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQ711250.1 GI:5460566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High Throughput
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                    to reverse of: AQ711250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              quality sequence stop: 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomLy chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="Plate=925 Col=8 Row=P"
/clone_lib="RPCI-11.Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                           157.50
1.445
63.743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ဂ
                                                                                                                                                                                                                                                                                                                                                                                                           Length: 171
Gaps: 7
Percent Identity: 32.164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 g
                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hood L
                                                                                                                                                                                                                                                                                         to:
                                                                                                                                                                                                                                                                                            538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 others
       404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
```

```
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_gss15:AZ078264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 nAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                193 AlaValLeuLeuIlePheSerLeuGlyArgHisThrArgGlnMetAr 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 laLeuLeuSerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMet 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256 ACATGGATCTCATGGCTTTAGAAATGCCAACACAGAAGCCCCATATAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 CCAGTTCTNTATGCTGAAGGACATAAAGACAGCATATCCCTCTGGCCACT 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        162 TTTGCTGCCTTCATGACAAATATGACATTTAGTTTACCTTACAGAAGTCA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 IleLysValPheLeuSerSerLeuLysPheHisIle.....ArgArgPh 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 erLeuIleLeu 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alAlaGluPheSerVal......ProLeuLeuIlePheLeuPhe 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CACCACACTAAAAAAGAGTANATCA...AAGATAAAGANAATTAGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt gAsnThrValAlaGlySerArgValProGlyArgGlyAlaProIleSerA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCACTTCTATGTTACTCATCTCTTTTACAAGCACACTCATCGGATGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCTTCTTGTCAACTTGGCATTAATATTTCCTCTAGCCATATNTGTGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          eIlePheLeuPhePheIleLeuValIleGlyIleTyrProSerGlyHisS 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGGTTATAATA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RPCI-23-399P19.TV RPCI-23 Mus musculus genomic clone RPCI-23-399P19
                                                                                                                                                   library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
plate: 399 row: P column: 19
                                                                                                                                                                                                                                                                                                                                      Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other_GSSs: RPCI-23-399P19.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zhao, S., Nierman, W., Feldblyum, T., Malek, J., She, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 644)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ078264.1 GI:7371163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and and Fraser, C.M
                                                                                                                                                                                                                                                                                             Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                               Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence.
                                                                                                                                     primer: T7
                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ďα
                                                                                                                                                                                                                                                                                                                                                                                              Research Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shatsman,S.,
K., Krol,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Akinret
```

```
BASE COUNT
ORIGIN
       seq_documentation_block: LOCUS BE033430
                                                                        seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-510-332-1 x AZ078264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AZ078264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                          433 TTTCTGTATTTATCTGTTCATCCTTTTCTTCTGGTTTTATGGAACAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 ArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerPheLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 rgHisThrArgGlnMetArgAsnThrValAlaGlySerArgValProGly 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 upheAlaVal.....LeuLeuLeuIlepheSerLeuGlyA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 ACAGAAGCACACATAAAAGCTATGAAAACTATGATGTCATTCCTTTTGTT 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 PheSerPheValAlaGluPheSerVal.....ProLeuLeuIlePheLe 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 MetIleLeuGlySerLeuLeuTyrValSerMetIleCysValPheHisSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 ATTGTCCTAGGCACACTCATGTATTTCATTTTATTTCTCATTTTATGAA
                                                                                                                                                                                                                                  GlyIleTyrProSerGlyH1sSerLeuIleLeuIleLeuGlyAsnProLy 283
                                                                                                                                                                                                                                                                                                                                                                                         CTTCATCATATATTATATTAGCAACATTATGCTTATTGTGGCAAGCTCCA 388
                                                                                                                                                         sLeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLysCys 297
                                                                                                                                                                                                                                                                                                TTCTTGACAATGTGGTTGCACAAATTTTCTCTTATAACCTA.....ATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rLysTyrAlaGlyPheMetValProTyrPheLeuArgLysPhe.....P 160
                                                                                                                                                                                                                                                                                                                                           euLysPheHisIleArgArgPheIlePheLeuPhePheIleLeuValIle 266
                                                                                                                                                                                                                                                                                                                                                                                                                      ....IleLeuTyrPheSerHisCysMetIleLysValPheLeuSerSerL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGAACAAAACACATTCCCTGTTTTAGATACTCTAAGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heSerGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIle 176
                                                                                                                 ATTGAAATGGACATTCCAGCATGTATTGAGAAAGCTGGTGTGT 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCACCTTAGGAGGATGAAACTACAGGGCATACATACCAAAGACATAAGC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ...GGTTTCTTAGTCTACCATAGCCTCTACAATGGGATTCTCATTTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATGATAGCTAAT.....AATTTTATCTACAAATGGACAAAAT 100
                                                                        gb_est66:BE033430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DHIOB electrocompetent cells (BRL Life Technologies). "a 114 c 101 g 237 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             150.00
1.456
56.906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RPCI-23-399P19"
/clone_lib="RPCI-23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
    1176
  ďq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 181
Gaps: 7
Percent Identity: 30.387
    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 644
  EST
                                                                                                                                                                                                          482
                                                                                                                                                                                                                                                                                                     432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
07-JUN-2000
```

```
alignment_block:
US-09-510-332-1 x BE033430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                   517
                                                                                                                                           467
                                                                                                                                                                                                             417 TCTTTTCTTTCTCTCTTTTTCATCTTTCTCTATTTCCTACTTTT
                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                             374
                                                                                                                                                                                                                                                                                                                                                                                                                             324 CTCTTCTATTATTTCTATATTCTTTATTCTTTTTCCTTTCTTTCTTTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                            95 uAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSerValArgH 112
                                                                                                         83
                                                                                                                                                                               72
                                                                                                                                                                                                                                             55 gIlePheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePheP 72
                                                                                                                                                                                                                                                                                                                           39
                                                                                                                                                                                                                                                                                                                                                                                                22
                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 LeuIleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePh
TTCTACTTTCCTTCCTTTTTTCTTT
                                                                                                                                         TTCATTC ........
                                                                                                                                                                                                                                                                                                                                                                                           eThrAsnGlyTleIleValValAsnGlyIleAspLeuIleLysHisA 39
                                                                   AlaIleLeuLeuPheIleAsnGluLeuGluLeuTrp.....Le 95
                                                                                                                                                                       he.....lleGluPheIleMetCysSerAlaAsnCys 82
                                                                                                                                                                                                                                                                                                                     rgLysMetAlaProLeuAspLeuLeuSerCysLeuAlaVal.SerAr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesembryanthemum crystallinum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnollophyta; eudicotyledons; core eudicots; Caryophyllidae;
Caryophyllales; Alzoaceae; Mesembryanthemum.

1 (bases 1 to 1176)
Bohnert, H. J. , Borchert, C., Brazille, S., Brooks, J., Eaton, M., Ferrea, H. Kawasaki, S., McCollough, A., Michalowski, C.B., Palacio, C.,
Scara, G., Wheeler, M. and Zepeda, G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Functional Genomics of Plant Stress Tolerance Unpublished (2000)
Contact: Michalowski,C.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ME01F08 ME Mesembryanthemum crystallinum cDNA 5' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bio Sciences West room 513, Tel: 520-621-7982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax: 520-621-1697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Arizona
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polyubiquitin, mRNĀ sequence.
BE033430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE033430.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ail: cbm@u.arizona.edu
open reading frame exists.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: BE033430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ωi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="5-6 weeks"
/note="grown in hydroponics,
Hoagland's); 6 h stress"
1 324 c 65 g 658 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mesembryanthemum
/db_xref="taxon:3544"
/clone_lib="ME"
/tissue_type="roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148.00
0.902
53.420
                                                                                                                                                                                                                                                                                     .CTTTCTTTTCTCTTTTCTTTTCTCTTTCTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GI:8328439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307
13
25.081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ 85721,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 crystallinum'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stress
. ATCTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
598
                                                                   566
                                                                                                                                                                                                               466
                                                                                                                                                                                                                                                                                     416
                                                                                                                                                                                                                                                                                                                                                                                                                                 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NaCl (in 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ç
```

```
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS B17827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_gss23:B17827
                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                 ERSION
                                                                                                                                                                 TITLE
                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1040 CTCCTTATTTCTTCCTTTCTTTA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 isproLeuPhelleTrpLeuLysMetArglleSerLysLeuValProTrp 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           129 MetIleLeuGlySerLeuLeuTyrValSerMet.IleCysValPheHisS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 oIleSerAlaLeuLeuSerIleLeuSerPhe..LeuIleLeuTyrPheSe 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 GlnMetArgAsnThrValAlaGlySerArgValProGlyArgGlyAlaPr 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCTTATCTTCTTCTTCTTCTTCTTCTTATTTTTTCCTTTA 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePh 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erLysTyr...AlaGlyPheMetValProTyrPheLeuArgLysPhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTATTCTCTTTTCTATCTTCTCATTTCTCTTTCTTTTTATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 heLeuPheAlaValLeuLeuLeuIlePheSerLeuGlyArgHisThrArg 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eSerPheValAlaGluPheSerValProLeu.....LeuIleP 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTCTTCATCTTCATTATTTATCCATCTTCTATTACT.....TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rHisCysMetIleLys.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGCTCTCTTATCTCTTCTTTCTTTCTTTCTCTTTATTACTC 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rGlyHisSerLeuIle 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTTTTCTTCTTTTCTATTCTTATTCCTCTCATCTTCTTATCTTCATCCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheLeuPhePheIleLeuValIleGly.....IleTyrProSe 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCATCTTCTCTTTTCATTTTTCTTTCCTCTCTATTTCCTCTCTCTCTTT 1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTCATTTCTTTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....valPheLeuSerSerLeuLysPheHisIleArgArgPheIle 258
                                                                                                                                                                                                                                                                                                                                                  sequence.
B17827
                                                                                                                                                                                                                                                                                                                                                                                         B17827 466 bp DNA GSS 347L19.TPB CIT978SKA1 Homo sapiens genomic
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 466)
Adams, M.D., Kelley, J.M., Rounsley, S.R. and Venter, J.C.
Use of a BAC End Sequence Database for Sequence-Ready Map Building Unpublished (1997)
Other_GSSs: 347119.TVB
                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                 B17827.1 GI:2125576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....TTATTTATC
                                             MD 20850,
                                                                                                                                                                                                                                                                                                                                                                                                clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244
                                                                                                                                                                                                                                                                                                                                                                                                A-347L19, DNA
```

```
alignment_block:
US-09-510-332-1 x B17827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
                                                                                                       VERSION
KEYWORDS
                                                                                                                                                                                               seq_documentation_block:
LOCUS BE734359
                                                                                                                                                                                                                                           seq_name: gb_est75:BE734359
                                                                                                                                                                           DEFINITION
                  REFERENCE
                                                                                        SOURCE
                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: B17827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                     ORGANISM
   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201 uGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerArgValP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 CAATCATGTATCCTTCATTCCACTCATTCCTGATTATGGGAAGTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174
                                                                                                                                                                                                                                                                                  321
                                                                                                                                                                                                                                                                                                                                                                                   266 leGlyIleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnPro 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 rLeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLeuVall 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTTATTTGCCATTTACTTTCTGTGTATAATC...ACATCAACTTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IleLeuTyr.....PheSerHisCysMetIleLysValPheLeuSerSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  roGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTGTAAACATCTCAAGAAGATGCGGCTCCATAGCAAAGGATCTCAAGATC
                                                                                                                                                                                                                                                                                                            LysLeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLysCys 297
                                                                                                                                                                                                                                                                                                                                                                                                                        :|||:::
TCTTAGGACACAGCAGAGCAAACTTGTACTCCTGCCTTTGCCAAACTGTTG
                                                                                                                                                                                                                                                                                  AAGCTAAAACAGACCTTTCTTTCAGTTTTGTGGCAGATGACATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: SP6 Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1544)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.
                                                                                                                                          mRNA sequence.
BE734359
                                                                                                                                                                         BE734359 1544 bp
601565606F1 NIH_MGC_21
                                                                                                                       BE734359.1 GI:10148351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               מ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Fibroblast"
/note="Vector: pBACl08r; Site_1: HindIII; Site_2: HindIII;
CalTech Human BAC Library Al"
a 108 c 82 g 141 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="A-347L19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147.50
1.967
65.217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="CIT978SKA1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity:
                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 466
                                                                                                                                                                             A EST 15-SEP-2000
sapiens cDNA clone IMAGE:3840529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
35.652
                                                                                                                                                                                                                                                                                       365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249
                                                                                                                                                                                                                                                                                                                                                                                                                                270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                                                                                                             320
                                                                                                                                                                                                   15-SEP-2000
                                                                                                                                                                                    ű
```

```
alignment_block:
US-09-510-332-1 x BE734359/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: BE734359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1148 CTTGTTTTGGTGTTTTTGTTTTGTCTCGTCTTTTGAGGGTTGCCTGGTT 1099
                                                                                                                                                                                                                                                                                                                                                                         1049 TETETTTTGTGGTGTGTTTCTGGTTTGTTGCTGTGTTCTTGTCGCTTTTT 1000
122 leSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSer 138
                                                                                                                                                                                                                                                                                 999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                                                                                      72 heIleGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIle 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22 eThrAsnGlyIleIleValValAsnGlyIleAspLeuIleLysHisA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCGTTTCT........
                                                                                                                         aLysValAlaSerValArgHisProLeuPheIleTrpLeuLysMetArgI 122
                                                                                                                                                                          AsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAl 105
                                                                                                                                                                                                                                                                       TTTTTCTGTTTTTTTT.........TTTTTCCTGTTTTGT 968
                                                                                                                                                                                                                                                                                                                                                                                                                     gIlePheLeuClnLeuPheIlePheTyrValAsnValIleValIlePheP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ······CTCTGTGTTGCGTGTCTTGGTGTTCTTGTT 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rgLysMetAlaProLeuAspLeuLeuLeuSerCysLeuAlaVal.SerAr 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuIleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePh 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov
Plate: LLCM830 row: 1 column: 02
High quality sequence stop: 54.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Ling Hong/Rubin Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ct: Robert Strausberg, Ph.D. (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="choriocarcinoma"
/lab_host="bHi0B (phage resistant)"
/note="organ: placenta; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the placetionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Callifornia, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
a 281 c 222 g 59 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           141.50
0.963
48.515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3840529"
/clone_lib="NIH_MGC_21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 303
Gaps: 18
Percent Identity: 26.403
                                                                          TTTTTTGTGTTGTCTTCGGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 1544
                                                                          886
                                                                                                                                                                            918
```

```
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS BF037592
                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est79:BF037592
                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 uIleLeuTyrPheSer......HisCysMetIleLysValPheLeu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264 uValIleGlyIleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155 eLeuArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThrL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 MetIleCysValPheHisSerLysTyrAlaGlyPheMetValProTyrPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   188 uIlePheLeuPheAlaValLeuLeuLeuIlePheSerLeuGlyArgHisT 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          885 TTTGTGGCTTGGTCTTTTTCTTCTTTTGGGGTTGTTTTTCTTTGTGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTGTTTTTG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaProIleSerAlaLeu.....LeuSerIleLeuSerPheLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          euAlaIleGlnIlePheSerPheValAlaGluPheSer.ValProLeuLe 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       snProLysLeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLysCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTTGTGTTGTTTT...TTTTGGTCTTTCCTCTTTGTTTTTGTTCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerSerLeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTGGTTTTTTTGGTTTCTTTCTCTCTTGTCTGTGTTTTGTGTTTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hrargGlnMetargasnThrValalaGlySerargValProGlyArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....TGTTTTTTTTTGTGTTG...TTCTCTTGTCTCTTTTGT
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1502)

NIH-MGC http://www.ncbi.nlm.nih.gov/MGC/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                    BF037592 1502 bp
601461160F1 NIH_MGC_66
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                       Email: Robert_Strausberg@nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                Contact: Robert Strausberg, Ph.D
Tel: (301) 496-1550
                                                                                                                                                                                    Unpublished (1999)
                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                 BF037592.1 GI:10745870
EST.
                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
BF037592
                                                                     cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ......TTCGGTTCT..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .TTTTTTTGTTTTCTGCTCTCTGT
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens cDNA clone IMAGE: 3864615 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234
                                                                       (LLNL)
```

þe

```
alignment_block:
US-09-510-332-1 x BF037592/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 135.50
Ratio: 0.852
Percent Similarity: 45.042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: BF037592 from: 1 to: 1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1022 CTCTCCCCCCCTCCGTTGCCTCTTGTCTCGCTCCCTGTCCACGTTCTCC 973
                                                                                                                                                                                                                                                                                                1166 TCCGGGGCGTGGCTGTTGTCTCTCGGATTCCTGGCTGCCGCGTGGTG 1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1316 TGTTCTTCGTCCTGTCGTCTCTCCGTCTTCCCGTTTCTCCTTGTCT 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1266 TTCTGCTTTTCCTTCTCTGTTGCTGTCTTGTTTGCTGTTTTCCGTCTGTT 1217
                                                                                                                                                               131 LeuGlySerLeuLeuTyrValSerMetIleCysValPheHisSerLysTy 147
                                                                                                                                                                                                                                       102 eTyrCysAlaLysValAlaSerValArgHisProLeu........... 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                     933 ..... PCTTTTGTCCTC.....TTCTTTTCT..... 913
                                                                               147 rAlaGlyPheMetValProTyrPheLeuArgLysPhePheSerGlnAsnA 164
164 laThrIleGlnLysGluAspThrLeu.................Ala 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 PheIlePheTyrValAsnValIleValIlePhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 euAspLeuLeuCerCysLeuAlaValSerArgIlePheLeuGlnLeu 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 eValValValAsnGlyIleAspLeuIleLysHisArgLysMetAlaProL 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 LeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIleIl 27
                                                                                                                                                                                                                                                                                                                                                                                                                           86 LeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPh 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTTCGTCTCTCGTTTCCTCCTCGCTGCTGGCTTC...... 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plate: LLCM593 row: g column: 16 High quality sequence stop: 59. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 666 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="adenocarcinoma"
/lab_bost="DH10B (phage-resistant)"
/note="Organ: ovary; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life Technologies.

301 c 405 g 130 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3864615"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 17
Percent Identity: 22.380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DES
                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                               SZZS
```

	High quality sequence stop: 148 Location/Qualifiers e 11652	EATURES sourc
Laboratory nsortium (LLNL) information can be L at: image.llnl.gov	obert_Strausberg@nih.gov rocurement: ATCC brary Preparation: Ling Hong/Rubin : brary Arrayed by: The I.M.A.G.E. Couencing by: Incyte Genomics, Inc. istribution: MGC clone distribution rough the I.M.A.G.E. Consortium/LLNI LCM52 row: m column: 20	
,	Tel: (301) 496-1550	OMMENT
ollection (MGC)	NIH-MGC http://www. National Institutes	
ita; Euteleostomi idae; Homo.	human. M Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebra Mammalia; Eutheria; Primates; Catarrhini; Homini 1 (bases 1 to 1652)	OURCE ORGANISM EFERENCE
E: 29000	N 6009433/9f1 NIH_MGC_1/ Homo Sapiens CDNA Clone mRNA sequence. BEZ50598 BE250598.1 GI:9120712 EST.	EFINITION CCESSION ERSION EXWORDS
JUL-2000	BE250598 1652 bp mRNA EST	
	gb_est68:BE250598	eq_name:
	PheLeuLeu 293 TTCCTTCTG 460	291 P 468 T
290 469	eulleLeuglyAsnProLysLeuLysGlnAsnAlaLysLys ::::: ::::: TCGTCTTAGCTCGCCCTCTCCTGCTCGCGCCCTCGCCTTCGTGTCGCTGC	277 e 518 T
519	TICGICTICCTITGTTCTCTCTCCTTCCCACCCCCCTCGCCTCG	568 C
227		1 0
274 569	PhePheIleLeuVallIleGlyIleTyrProSerGlyHisSer	61
260	erSerLeuLysPheHisIleArgArgPheIlePheLeu 	248 e 668 C
248 669	LeuIleLeuTyrPheSerHisCysMetIleLysValPheLeuS	234 . 718 T
233	IleSerAlaLeuLeuSerIleLeuSerPhe	224 I 768 C
769	.CTTTGGTCTCGTGTTCCTGTCCCG	
223	gGlyAlaPro	207 1
207 793	eLeuPheAlaValLeuLeuLeuIlePheSerLeuGlyArgHisThrArgG TCTGTTCCTGTTTATTTTCTTTCTT	190 e 817 T
190	IleGlnIlePheSerPheValAlaGluPheSerValProLeuLeuIlePh :::::: :::: :::::: CTTCGGTCCTTCGCTTTCCTCTTCTTCTCTGCGTCGTTCTGTT	174 I 867 C
868		912 .

eostomí;

194	178 erphevalAlaGlupheServalproLeuLeuIlepheLeupheAlaval
178 880	161 rGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheS
930	150 PheMetValProTyrPheLeuArgLysPhe
149 980	139 etlleCysValPheHisSerLysTyrAlaGly:::
139	122 eSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSerM
122	106 LysValAlaSerValArgHisProLeuPheIleTrpLeuLysMetArgIl 1081 CTTGTTATT
105 1082	89 snGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAla 1093TTCTATTGTTTC
89 1094	72 eIleGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleA
72	56 IlePheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePh ::: ::: ::: :::::::::::::::::
55 1190	39 rgLysMetAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArg
39 1230	22 eThrAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisA :::::: ::: :::::
22 1280	6 LeuileileTyrPheLeuLeuAlaValileGlnPheLeuLeuGlyIlePh ::: 1329 GTTATTATATATCATCTGATTCGTTGTGTGTTCATTGTTGGGGGCGTGG
	Align seg 1/1 to reverse of: BE250598 from: 1 to: 1652
	alignment_block: US-09-510-332-1 x BE250598/rev
	alignment_scores: Quality: 135.50 Length: 304 Ratio: 0.948 Gaps: 11 Percent Similarity: 47.039 Percent Identity: 24.671
ming. ming the tes using the tes velected >500bp constructed by constructed by synthesis kit e Technologies)."	/db_xref="taxon:9606" /clone=lib="NIH_MGC_17" /clone=lib="NIH_MGC_17" /tissue_type="rhabdomyosarcoma" /tissue_type="rhabdomyosarcoma" /tissue_type="Thabdomyosarcoma" /tisue_type="Thabdomyosarcoma" /tisue_type="Thabdomyosar
	/organism="Homo sapiens"

	276 IleLeuIleLeu 279 ::: ::: 559 TTGCTAGTGTTG 548
275 560	263 leLeuVallleGlyIleTyrProSerGlyHisSerLeu
263 610	253 s
253 660	237. TyrPheSerHisCysMetIleLysValPheLeuSerSerLeuLysPheHi ::: :::
236 698	220 rgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerPheLeuIleLeu :::
220 745	211 rValAlaGlySerArgValProGlyA :::: 794 GCTTGTTCTGTGTTACTTTCTCCTACATGTGCTTCTGGTGCTTCTGGTA
211 795	195 LeuLeuIlePheSerLeuGlyArgHisThrArgGlnMetArgAsnTh ::: ::: 844 TCTCTTTGTTTCTCTTTTCTCTTTTGTGTCCTCTGTCTTCCGCTCCGT
845	879 TTTCGCTTTGTTTTTTTCTGTTTTGTTTTTCCTTG 845

THIS PAGE BLANK (USPTO)

```
9b_htg15:AC068649
9b_pr4:AF227137
9b_ro:AF240768
9b_htg16:AC073342
9b_htg16:AC073264
9b_htg17:AC01881
9b_htg7:AC01861
9b_htg18:AC079625
9b_pr3:AC010176
                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_htg5:AC016145
gb_pr2:AC006518
gb_pr4:AF227135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               욧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_rc:AF227140
gb_htg4:AC013470
gb_pr2:AC005541
gb_pr4:AF227130
gb_pr4:AF227139
gb_pr4:AF227133
gb_pr4:AF227133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         search information block:
Query: US-09-510-332-1
Query length: 299
gb_ro:AF227146
gb_pr4:AF227132
gb_ro:AF240765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database sequences: 1118133
Database length: -1736092196
Search time (sec): 1081.220000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Date: Mar 15,
                                                                                                                                                                                                                                                                                                                         gb_htg1:AC020619
gb_htg10:AC024164
gb_pr4:AF227136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database:
                                                                                                                                                                                                                                                                                                                                                                                                               gb_htg16:AC073342
gb_htg15:AC068649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -MODEL-frame+_p2n.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool/US09510332/runat_06032001_093637_13632/app_query.fasta_1.359
-Q-/cgn2_1/USPTO_spool/US09510332/runat_06032001_093637_13632/app_query.fasta_1.359
-DB-GenEmbl -QRMF-fastap -SUFFIX-rge -GAPOP-12.000 -GAPEXT-4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP-4.500
-QGAPEXT=0.000 -YGAPOP-10.000 -YGAPEXT=0.500 -FGAPOP-6.000
-FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500 -DELOP-6.000
-DELEXT=7.000 -START=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN=200 -THR_SCORE-pct -THR_MAX-100 -THR_MIN=0
-ALIGN-15 -MODE-LOCAL -OUTFMT-pfs -NORM-ext -MINLEN-0
-MAXLEN-2000000000 -USER-US09510332_eCGN1_1_4621 -NCPU=6
-ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
                                                              gb_htg3:AC011654
gb_htg17:AC073647
                                                                                                                                                                                                                                                                                                                                                                           gb_ro:AF240766
                                                                                                                                                                                                                                                                                                                                                                                           gb_htg10:AC024156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score_list:
                                                                                                                    gb_htg7:AC018851
gb_htg7:AC018630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       b_htg13:AC034214
                                                                                                gb_ro:AF227144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         b_ro:AF227149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of: US-09-510-332-1 to: GenEmbl:*
                                                                                                                                                        ro:AF227145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001 1:47 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1521.00
1521.00
1516.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          orig
                                                                                                                                                                                                                                                                                                                                                                                               371.50
371.50
371.50
371.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     434.50
405.00
                                                                                                                                                                                                                                          369.00
364.00
358.00
358.00
356.00
355.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 376.
376.
376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405.
376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         438.50
                                                                    333.00
331.50
327.50
325.50
                                                                                                                                                                                          .500
                                                                                                                                                                                                                                                                                                                                                                                                                                  .50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZScore
1807.51
1765.35
1758.77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       931.63
913.87
                                                                                                                                                                                                                                                                                                                                                                                             402.43
402.23
401.67
                                                                                                                                                                                                                                                                                                                                                                                                                                               408.05
407.49
446.22
                                                                                                                                                                                                                                                                          443.68
392.35
390.19
390.38
430.38
386.25
428.12
427.39
   376.22
371.37
371.37
371.04
371.04
367.73
367.73
361.85
361.85
361.85
361.85
361.85
361.85
361.85
361.85
361.85
361.85
361.85
361.85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             out_format : pfs
                                                                                                                                      1. 2e-18
6. 7e-19
6. 7e-19
8. 4e-17
5. 3e-17
7. 5e-14
1. 1e-14
1. 1e-14
2. 9e-14
3. 0e-14
3. 0e-14
3. 0e-14
3. 0e-14
1. 1e-13
1. 4e-13
8. 2e-16
1. 1e-15
7. 7e-13
1. 2e-15
7. 7e-13
1. 2e-12
2. 3e-12
2. 3e-12
1. 5e-12
2. 3e-13
1. 4e-13
1. 4e-13
2. 3e-13
2. 3e-13
2. 3e-13
2. 3e-13
2. 3e-13
2. 3e-13
3. 6e-14
2. 3e-13
3. 6e-14
2. 3e-13
3. 6e-14
2. 3e-13
3. 6e-14
3. 6e-12
3. 6e-13
   1.3e-11
4.5e-14
2.3e-11
3.3e-11
3.8e-13
4.2e-13
5.0e-13
5.7e-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EScore
1.6e-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.8e-44
9.6e-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Len | Documentation
900 | AF227119 Homo sapiens candidate
132953 | AC003015 Human BAC clone GSI
143719 | AC026787 Homo sapiens chromo
141747 | AC034214 Homo sapiens chromo
                                                                                                                                                                                                                                                                                                                                                                                                                82419
930 !
957 !
162553
173735
939 !
168200
172167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1008
1008
180438
110626
951
                                                                                                                                                                                                                                                                              256629
250463
924 !
172167
912 !
927 !
                   184034
200128
160326
180736
202103
945 !
162380
213227
918 !
168197
173000
927 !
930 !
                                                                                                                                                                                                                                                              168200
                                                                                                                                                                                                                                                                                                                                                                                                184034
              33 i ACO10145 Homo Sapiens chrome
35 i ACO10518 Homo Sapiens chrome
36 i ACO10518 Homo Sapiens candidate
100 i ACO10515 Homo Sapiens chrome
37 i ACO168649 Homo Sapiens chrome
38 i ACO124156 Homo Sapiens chrome
39 i ACO24156 Homo Sapiens chrome
39 i ACO26159 Mus musculus clone
30 i ACO26154 Homo Sapiens candidate
30 i ACO27156 Homo Sapiens candidate
31 i ACO27137 Homo Sapiens candidate
32 i ACO27342 Homo Sapiens chrome
33 i ACO17342 Homo Sapiens chrome
34 i ACO73264 Homo Sapiens chrome
35 i ACO17356 Homo Sapiens chrome
36 i ACO17356 Homo Sapiens chrome
37 i ACO11851 Homo Sapiens chrome
38 i ACO11076 Homo Sapiens chrome
39 i ACO11851 Homo Sapiens chrome
30 i ACO11851 Homo Sapiens chrome
30 i ACO11851 Homo Sapiens clone
31 i ACO11851 Homo Sapiens clone
32 i ACO11851 Homo Sapiens clone
33 i ACO11851 Homo Sapiens clone
34 i ACO27344 Rattus norvegicus cand
35 i ACO11654 Homo Sapiens clone
36 i ACO11654 Homo Sapiens clone
37 i ACO11654 Homo Sapiens clone
38 i ACO13647 Homo Sapiens clone
39 i ACO1765 Pattus norvegicus cand
30 i ACO1765 Pattus norvegicus cand
31 i ACO1765 Pattus norvegicus cand
31 i ACO1765 Pattus norvegicus cand
31 i ACO1765 Pattus norvegicus cand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! AF227130 Homo sapiens candidate
9 ! AC004979 Homo sapiens PAC clo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ! AF227149 Mus musculus candidat
! AF227140 Rattus norvegicus can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF227134 Homo sapiens candidate AF227133 Homo sapiens candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ! AC013470 Homo sapiens chromo AC005541 Homo sapiens clone
       AF240765 Rattus
       norvegicus
                                                                                                                                                                                                                                                                                                                  primer_bind
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_pr4:AF227139
gb_pr1:AC004838
gb_htg16:AC073311
gb_pr4:AF227138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
          51
                                          17
                                                                           1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2022257
```

```
seq_documentation_block:
LOCUS AF227129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_pr4:AF227129
                                                                                                                              alignment_block:
US-09-510-332-1 x AF227129
                                                                                                   Align seg 1/1 to: AF227129
                                                                                                                                                                   Quality: 1521.00
Ratio: 5.087
Percent Similarity: 100.000
                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 900)

Adler, E., Hoon, M.A., Mueller, K.L., Chandrashekar, J. Puha V. Zuker, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens candidate AF227129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (21-JAN-2000) NIDCR,
Drive, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF227129.1 GI:7262604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adler, E., Hoon, M.A., Mueller, K.L., and Zuker, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A novel family of mammalian taste receptors cell 100 (6), 693-702 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 900)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 (6), 693-702
                                                                                                                                                                                                                                                                                                       /product="candidate taste receptor T2R1" 881. .900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="5p15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                313.00
313.00
311.00
310.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 900
                                                                                                                                                                                                                                                             . .900
203 c
                                                                                                       from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  377.55
334.54
331.53
373.87
                                                                                                                                                                     Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA PRI
taste receptor T2R1
                                                                                                                                                                                                                                                             172 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.1e-13
1.8e-10
2.6e-10
1.1e-12
                                                                                                         to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH,
                                                                                                                                                                                                                                                               H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chandrashekar, J., Ryba, N.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chandrashekar, J., Ryba, N.J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bldg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    876 !
142992
154364
954 !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC004838 Homo sapiens PAC AC073311 Homo sapiens chr
AF227138 Homo sapiens candid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF227139 Homo sapiens candid

| AC004838 Homo sapiens PAC

| AC073311 Homo sapiens chr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Room 1N106, 10 Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete
        100
                                                        50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAR-2000
complete cds
```

```
seq_name:
                                                                                                                           751
                                                                                                                                                 251
                                                                                                                                                                          701
                                                                                                                                                                                                234
                                                                                                                                                                                                                          651
                                                                                                                                                                                                                                                                          601
                                                                                                                                                                                                                                                                                                 201
                                                                                                                                                                                                                                                                                                                          551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 ervalProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIlepheSer
                                                                                                                                                                                                                                                                                                                                                                        501
                                                                                                                                                                                                                                                                                                                                                                                                                       451
                                                                                                                                                                                                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 pLeuLysMetArgIléSerLysLeuValProTrpMetIleLeuGlySerL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      151
                      yIleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnProLysL 284
                                                                                                                    nLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaGluPheS 184
                                                                       TATATACCCTTCTGGACACTCTCTCATCTTAATTTTAGGAAATCCTAAAT
                                                                                                                                                                                                                      TCCTGGCAGGGGTGCACCCATCAGCGCGTTGCTGTCTATCCTGTCCTTCC
                                                                                                                                                                                                                                   lProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerPheL 234
                                                                                                                                                                                                                                                                      CTGGGGAGGCACACCGGCAAATGAGAAACACAGTGGCCGGCAGCAGGGT
                                                                                                                                                                                                                                                                                 LeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerArgVa
                                                                                                                                                                                                                                                                                                                      CAGTGCCATTGCTTATCTTCCTTTTTGCTGTTTTGCTCTTGATTTTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValPheTyrCysAlaLysValAlaSerValArgH1sProLeuPheIleTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly
                                                                                                                                                                       ATGGTCCCATACTTCCTAAGGAAATTTTTCTCCCAAAATGCCACAATTCA 500
                                                                                                                                                                                                                                                                                                                                                                                                                                MetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIleG1 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGAAGATGAGGATATCCAAGCTGGTCCCCATGGATGATCCTGGGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTCTTATTTATAAATGAATTGGAACTTTGGCTTGCCACATGGCTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTTTTCTATTGTGCCAAGGTTGCCAGCGTCCGTCACCCACTCTTCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTGGCAGTTTCTAGAATTTTTCTGCAGTTGTTCATCTTCTACGTTAATGT
gb_pr1:AC003015
                                                                                                                                                                      750
                                                                                                                                                                                             250
                                                                                                                                                                                                                      700
                                                                                                                                                                                                                                                                       650
                                                                                                                                                                                                                                                                                                                      600
                                                                                                                                                                                                                                                                                                                                             200
                                                                                                                                                                                                                                                                                                                                                                      550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                                             217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150
```

seq_documentation_block:
LOCUS AC003015 1:
DEFINITION Human BAC clo
ACCESSION AC003015

Human BAC clone

132953 bp DNA clone GS1-113H23

from

5p15

source

VERSION KEYWORDS

AC003015.1 GI:2547255

```
.2
                                                                           complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap
                                                                                       This clone contains (NID:9454585).
                                                                                                                                                        The clone sequenced to the left is GS1-330J10, Actual start of this clone is at base position actual end is at 132953 of GS1-113H23.
                                                                                                                                                                                                                                                                                                   (http://www.genomesystems.com)
Cell line: lymphoblastoid
Haplotypes: two
VECTOR: pBeloBAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mapping information for this clone was also provided by Dr. Michael Lovett, Departments of Otorhinolaryngology, Molecular Biology and Oncology, University of Texas Southwestern Medical Center, Dallas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (04-FEB-2000) Department of University, 4444 Forest Park Avenue, 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (03-FEB-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Direct Submission
Office (20-OCT-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
3 (bases 1 to 132953)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 132953)
Wamsley,P., Kramer,J., Elliott,G. and O'Brien,D.
The sequence of H. sapiens BAC clone GS1-113H23
                                                                                                                                                                                                                                                                                                                                                                                             This clone is from the first BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between neighboring data submissions.
                                                                                                                                                                                                                                                                               Selection:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Waterston, R.
                                                                                                                                                                                                                               VEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lversity, 4444 Forest (bases 1 to 132953)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 132953)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name: H_GS113H23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Washington University Genome (Center code: WUGSC Web site: http://genome.wustl.edu/gsc Contact: sapiens@watson.wustl.edu
clone contains polymorphisms with GS1-330J10
    Location/Qualifiers
    . 1. .132953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    information for this clone on, Department of Genetics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           St. Louis
                                                                                                                                                                                                                                                                             chloramphenicol
                                                                                                               STS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>₩</u>
                                                                                                               HSC022YA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Genetics, Park Avenue, St. Louis,
                                                                                                               (NID:g1235481)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 was provided by Dr. John D. Washington University School
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          f Genetics,
St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                          from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                             Genome
                                                                                                                                                                                 200 bp overlap.
1 of GS1-113H23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
Missouri 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
Missouri 6
                                                                                                               and HS268ZD9
                                                                                                                                                                                                                                                                                                                                                                                             Systems,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63108,
```

of.

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(359. .853)
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(20. .194)
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(4322. .4351)
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(3640.
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="GSBAC1"
/map="5p15.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt__tun=
complement(5046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(3820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(3764
/rpt_family="L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="GS1-113H23"
                                           7rpt_1
31649
                                                                                                                                                                                                                                                               complement(14607..17154)
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                           complement(9591;
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(7459.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (6985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (687)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(5527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(4444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="ALU"
complement'...
                                                                                                                                                                                                                                                                                     complement(11563. .14264)
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                 complement (9854.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rpt_family="L1"
                                                                                                                                                                     complement(26967./rpt_family="L1"
                                                                                                                                                                                                                               complement (21565.
                                                                                                                                                                                                                                                      complement(17883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rpt_family="L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="L1"
                     /rpt_family-"L1"
33991 .34027
                                                                                        complement (30225.
                                                                                                               complement(29892.
                                                                                                                                      complement(29140.
                                                                                                    'rpt_family="L1"
                                                                                                                         /rpt_family="Ll"
                                                                                                                                                                                                                                          rpt_family="L1"
                                                                                                                                                                                                                                                                                                                        rpt_family="L1"
1262. .11306
                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="L1"
                                                                                                                                                                                            rpt_family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                               rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                     _family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _family="L1"
                                                                           _family="L1"
                                                                                                                                                                                                                   family="L1"
                                                                                                                                                 _family="L1"
family="L1"
                                                                                                                                                              29051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . .3788)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .8612)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .7389)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .6871)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .5122)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4464)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .3667)
                                                                                                                                                                                                                                                                                                                                                 .9961)
                                                                                                                                                                                                                                                                                                                                                                         .9823)
                                                                                                                                                                                                                                                      .17902)
                                                                                                                 .30124)
                                                                                                                                                                                   .27276)
                                                                                                                                                                                                                                .21588)
                                                                                                                                        .29165)
                                                                                         .30258)
                                                                                                                                                                                      alignment_block:
US-09-510-332-1 x AC003015
                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                     Quality: 1521.00
Ratio: 5.087
Percent Similarity: 100.000
                                                                                                                                                              Align seg 1/1 to: AC003015
                                                                    54951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                34
  51 LeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa 67
                        /rpt_family="L1"
complement(36832.
/rpt_family="L1"
39878...39924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(44871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(41297)/rpt_family="MER"
                                                                                                                                                                                                                                                                               complement (63786. /rpt_family="ALU"
                                                                                                                                                                                                                                                                                                      /rpt_family="L1"
complement(63757
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                         /rpt_family="L1" 62686. .62745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="MER"
complement(52291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(45907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(45830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(45255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(45153
                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="L1"
complement(59606
                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="ALU"
complement(58482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpt_family="MER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'rpt_family="MER'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'rpt_family="MER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family="L1"
1617. .51660
                                                                                                                                                                                                                                                                                                                                                                           _family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family="MER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _family="MER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family-"L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family="MER"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family="MER"
                                                                                                                                                                                                                                                                                                                                                                                                                          _famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .54297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .52459
                                                                                                                                                                                                                                                                                                                                                                                                                                                              .58479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .53635
                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ly-"L1"
                                                                                                                                                                                                                     Length: 299
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                          Ly="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .45882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .44963)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .44621)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .46229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .45761)
                                                                                                                                                                 to: 132953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .52521)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .45205)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .41751)
                                                                                                                                                                                                                                                                                              .64077)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36880)
                                                                                                                                                                                                                                                                                                                    .63785)
                                                                                                                                                                                                                                                                                                                                                                                          .59897)
                                                                                                                                                                                                                                                                                                                                                                                                                                       . 58529)
                                                                           54950
                              55000
```

repeat_region
repeat_region
repeat_region
repeat_region
repeat_region
repeat_region

repeat_region

repeat_region repeat_region repeat_region

repeat_region

repeat_region

repeat_region repeat_region

repeat_region repeat_region

repeat_region
repeat_region
repeat_region
repeat_region
repeat_region
repeat_region

repeat_region

repeat_region

repeat_region repeat_region repeat_region
repeat_region
repeat_region
repeat_region
repeat_region

```
seq_documentation_block:
LOCUS AC026787 1.
                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                 seq_name: gb_htgl2:AC026787
                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yIleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnProLysL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATATACCCTTCTGGACACTCTCTCATCTTAATTTTAGGAAATCCTAAAT 55700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTGGCAGGGGTGCACCCATCAGCGCGTTGCTGTCTATCCTGTCCTTCC 55550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerArgVa 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerPheL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGGGGAGGCACACCCGGCAAATGAGAAACACAGTGGCCGGCAGCAGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIleG1 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTGAAGATGAGGATATCCAAGCTGGTCCCATGGATGATCCTGGGGTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValPheTyrCysAlaLy9ValAlaSerValArgHisProLeuPheIleTr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGGTCCCATACTTCCTAAGGAAATTTTTCTCCCAAAATGCCACAATTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLeuLySMetArgIleSerLySLeuValProTrpMetIleLeuGlySerL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTTTCTATTGTGCCAAGGTTGCCAGCGTCCGTCACCCACTCTTCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GATTGTTATCTTCATAGAATTCATCATGTGTTCTGCGAATTGTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lileValilePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 143719)
                                                                                                                                                                  Homo sapiens chromosome 5 cl
SEQUENCE, 10 ordered pieces
                                                               Homo sapiens
                                                                                                   AC026787.3 GI:9256685
HTG; HTGS_PHASE2; HTGS_DRAFT
                                                                                                                                                                                                                143719 bp
                                                                                                                                                                                         DNA HTG
5 clone CTD-2143L24,
                                                                                                                                                                                         18-JUL-2000
WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55150
           alignment_block:
US-09-510-332-1 x AC026787
                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                       * provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

1 1768 contig of 1768 bp in length

1869 18093 contig of 16225 bp in length

* 18194 54185 contig of 35992 bp in length

* 54186 54285 gap of unknown length

* 54186 54285; gap of unknown length

* 84033 84132 gap of unknown length

* 84033 84142 contig of 29747 bp in length

* 84133 89414 contig of 5282 bp in length

* 89415 9745; contig of 7943 bp in length

* 89515 9745; contig of 7943 bp in length

* 132197 134948; contig of 34539 bp in length

* 132197 134948; contig of 2752 bp in length

* 132197 134948; contig of 2752 bp in length

* 13247 139346; gap of unknown length
                                                                        Quality: 1516.00
Ratio: 5.070
nilarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 136146 bases at least 040
Consensus quality: 1421397 bases at least 020
Consensus quality: 142269 bases at least 020
Estimated insert size: 145000; pulse field gel estimation
Estimated insert size: 143119; sum-of-contigs estimation
Quality coverage: 5.41 in 020 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 10 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Project Information Center Project Name: 682749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOE Joint Genome Institute.
Sequencing of Human Chromos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: CITB-H1_2143L24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 143719)
DOE Joint Genome Institute.
                                                                                                                                                                                                                               44478
                                                                                                                                                                                                                               a
                                                                                                                                                                                                                      /clone="CTD-2143L24"
/clone_lib="CalTech human
28860 c 28265 g 41210
                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Chromosome
                                                                 Length: 299
Gaps: 0
Percent Identity: 99.666
                                                                                                                                                                                                                           t
t
                                                                                                                                                                                                                         library D"
906 others
```

VERSION KEYWORDS

ACCESSION

55601

284

55551

234

55501

55451

55401

55201

117

151

55151

55101

84

55051

67

55001

REFERENCE

to: AC026787

from: 1

to:

```
Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4567
                                                                                                                                                                                                                                                                                                                                                                                                            4817
                                                                                                                                                                                                                                                                                                                                                                                                                                                4767 TTCTCTTATTATAAATGAATTGGAACTTTGGCTTGCCACATGGCTCGGC
                                                                                                                                                                                                                                                            5017
                                                                                                                                                                                                                                                                                                                                    4917
                                                                                                                                                                                                                         5067
                                                                                                            5217
                                                                                                                                                5167
                                                                                                                                                                                     5117
                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
                                                                                                                                                                                                      201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeualaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGCTAGAGTCTCACCTCATTATCTATTTTCTTCTTGCAGTGATACAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | IlleValIlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GATTGTTATCTTCATAGAATTCATCATGTGTTCTGCGAATTGTGCAA 4766
                                                                                                                                                                                                                                                            nLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaGluPheS 184
||||||||||||||||||||
| AAAAGAAGATACACTGGCTATACAGATTTTCTCTTTTGTTGCTGAGTTCT 5066
                                                                                                                                                                                                                                                                                                          MetValProTyrPheLeuÀrgLysPhePheSerGlnAsnAlaThrIleG1 167
ATGGTCCCATACTTCCTAAGGAAATTTTTCTCCCAAAATGCCACAATTCA 5016
                                                                                                            TGATCCTCTACTTCTCCCACTGCATGATAAAAGTTTTTCTCTCTTCTTCTA
                                                                                                                     euIleLeuTyrPheSerHisCysMetIleLysValPheLeuSerSerLeu 250
                                                                                                                                                TCCTGGCAGGGTGCACCCATCAGCGCGTTGCTGTCTATCCTGTCCTTCC
                                                                                                                                                          4566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                            4916
                                                                                                                                                                                                                                                                                                                                                                                                               4866
                                                                                                                                                                                                                                                                                                                                                                                                                                                   4816
                                                                                                               5266
                                                                                                                                                   5216
                                                                                                                                                                     234
```

```
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_htgl3:AC034214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                      Consensus quality: 129482 bases at least Q40
Consensus quality: 137633 bases at least Q30
Consensus quality: 139230 bases at least Q30
Consensus quality: 139230 bases at least Q30
Estimated insert size: 128750; agarose-fp estimation
Estimated insert size: 141047; sum-of-contigs estimation
Quality coverage: 4.64 in Q20 bases; agarose-fp estimation
Quality coverage: 4.64 in Q20 bases; sum-of-contigs estimation

**NOTE: This is a 'working draft' sequence. It currently

**consists of 16 contigs Gaps between the contigs

**are represented as runs of N. The order of the pieces

**is believed to be correct as given, however the sizes

**of the gaps between them are based on estimates that have

**provided by the submittor.

**This sequence will be replaced

**by the finished sequence as soon as it is available and

**the accession number will be preserved.

1 21583 21682: gap of unknown length

** 21583 34005: contig of 12582 bp in length

** 3106 34105: gap of unknown length

** 3106 37105: contig of 3000 bp in length

** 37206 39674: contig of 2469 bp in length

** 37206 39674: contig of 2469 bp in length

** 37206 39774: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG 18-JUL-2
Homo sapiens chromosome 5 clone CTD-2001E22, WORKING DRAFT
SEQUENCE, 16 ordered pieces.
AC034214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (05-APR-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced 91:7712070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 141747)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 141747)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC034214.4 GI:9256725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center Project Name: 628051
Center clone name: CITB-H1_2001E22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.jgi.doe.gov
73886
73986
92579
92679
103696
103796
                                                                                                                                                                                                                                                                           21583
21683
34006
34106
37106
37206
39675
39775
                                                                                                                 46529
46629
52638
52738
57098
57198
57198
58514
58614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa;
                  73985:
92578:
92678:
103695:
103795:
                                                                                                                                         5861:
                                                                                                                                                            58513:
                                                                                                                                                                                                                                                                               46528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                   7: gap of unknown length
3: contig of 1316 bp in length
3: gap of unknown length
5: contig of 15272 bp in length
6: gap of unknown length
6: gap of unknown length
6: contig of 18593 bp in length
6: gap of unknown length
6: contig of 11017 bp in length
                                                                                                                                                                                             gap of unknown contig of 6754 gap of unknown contig of 6009 gap of unknown contig of 4360
  gap of contig
                                                                                                                                                                                               f unknown
g of 6009
f unknown
g of 4360
  unknown
of 2437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                    bp in
                                                                                                                                                                                                                                          length
bp in length
                                                                                                                                                                                                                                                                                  bp in
  ďα
                                                                                                                                                                                                                    length
                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                             length
    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JUL-2000
```

```
alignment_block:
US-09-510-332-1 x AC034214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
Source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AC034214 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 1170.50
Ratio: 4.417
Percent Similarity: 87.748
39557
                                                                                                                                   39508
                                                                                                                                                                        39408
                                                                                                                                                                                                                                                           134
                                                                                                                                                         117
                                                                                                                                                                                                                                           84
                                                                                   GlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaGluPh 183
                                                                                                                              GTTGAAGATGAGGATATCCAAGCTGGTCCCCATGGATGATCCT.GGGTCTC 39556
                                                                                                                                           PLeuLysMetArgIleSerLysLeuValProTrpMetIleLeuGlySerL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41436 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106233
106333
121674
121774
124115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .141747
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CTD-2001E22"
/clone="CTD-201Tech human BAC library D"
/28372 c 28509 g 41923 t 1507 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106332: gap of unknown length
121673: contig of 15341 bp in length
121773: gap of unknown length
124114: contig of 2341 bp in length
124214: gap of unknown length
131887: contig of 7673 bp in length
131987: gap of unknown length
141747: contig of 9760 bp in length.
141747: contig of 9760 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 302
Gaps: 4
Percent Identity: 84.768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 141747
                                                                                                                                                                          39507
                                                                                                                                                                                                                                                                                                                                                                                            39257
```

BASE COUNT ORIGIN		CDS	TITLE JOURNAL FEATURES Sourc	TITLE JOURNAL MEDLINE REFERENCE AUTHORS	SOURCE ORGANISM ORGANISM REFERENCE AUTHORS	seq_documen LOCUS DEFINITION ACCESSION VERSION KEYWORDS	seq_name:	283 y 39978 <i>l</i>	266 (39928 :	250 I 39878 (39828	217 · 39779 ·	39729	39704	183
224 a 252 c 209 g 323 t	/note="G protein-coupled receptor" /codon_start= /codon_start= /product="candidate taste receptor T2R19" /protein_1d="AAF43922.1" /protein_1d="AAF43922.1" /db_xref="G1:726245" /translation="MMEGHMLFFLLVVVQFLTGVLANGLIVVVNAIDLIMWKKMAPL /translation="MMEGHMLFFLLVVVQFLTGVLANGLIVVVNAIDLIMWKKMAPL /translation="MMEGHMLFFLLVVVQFLTGVTFYISRETSELPKQITISFF YCAKIATIPHPLFLMLKMRISRLVPWLILASVVYVTVTFIHSRETSELPKQITEPSF SKNTTRVRPAHATLLSVFVFGLTLFPLLFTVAVLLLLSSLMHHSRQMFMVGTREPSR HALVSAMLSILSFLILYLSHDMVAVLICTQGLHFGSRTFAFCLLVIGMYPSLHSIVLI LGNPKLKRNAKTFIVHCKCCHCARAWVTSRNPRLSDLPVPATHHSANKTSCSEACIMP S"	m="Mus musculus" "129/svJ" ="taxon:10090"	Direct Submission Submitted (21-JAN-2000) NIDCR, N Drive, Bethesda, MD 20892, USA Location/Qualifiers e 1, 1008	A novel family of mammalian taste receptors Cell 100 (6), 693-702 (2000) 20222571 Chases I to 1008) Adler, E., Hoon, M.A., Mueller, K.L., Chandrashekar, J., Ryba, N.J.P. and Zuker, C.S.	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; C Mammalia; Eutheria; Rodentia; S 1 (bases 1 to 1008) Adler, E., Hoon, M.A., Mueller, K. Zuker, C.S.	antation_block: AF227149 1008 bp DNA ROD 18-MAR-2000 N Mus musculus candidate taste receptor T2R19 gene, complete cds. AF227149 AF227149.1 GI:7262644	gb_ro:AF227149	ysLeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLysCysCysGln 299 	eGlyIleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnProL 283 	LeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLeuValI1 266	heLeuIleLeuTyrPheSerHisCysMetIleLysValPheLeuSerSer 249 	ValProGly.ArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerP 233 	erLeuGlyArgHisThrargGlnMetArgAsnThrValAlaGlySerArg 216::::::::::::::::::::::::::::::::::::		eSerValProLeuLeuIlePheLeuPheAlaValLeuLeuIlePheS 200

```
alignment_block:
US-09-510-332-1 x AF227149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AF227149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                          451
                                                                                                                                                                                                                                                                                                                                                                                                           151
                                                                                                                                                                                                                                                                                                                                                                                                                                           401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 TTGTCTACATTATAAACGAACTGAGTCTCTGGTTTGCCACATGGCTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       101
                                                                                                                                                                                                                                             545
                                                                                                                                                                                                                                                                                                           501
                                                                                                                                                                                                                                                                                                                                           166
                                                                                                               642
                                                                                                                                                                                                                                                                            183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                             200
                 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spLeuIleLysHisArgLysMetAlaProLeuAspLeuLeuLeuSerCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTCTATCCTGTTTGGTGAGACACACGTTATTTGCTGACAATGTTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTAACTGGGGTCTTGGCAAATGGCCTCATTGTGGTTGTCAATGCCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGATGGAAGGTCATATGCTCTTCTTCCTTCTGGTCGTGGTAGTGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh
                                                                                                                                                                                                                                            TCACACTACCATTTCTCATCTTCACTGTTGCTGTTCTGCTCTTGTTGTCC 594
                                                                                                                                                                                                                                                                                                                                                                         pLeuLysmetArgIleSerLysLeuValProTrpMetIleLeuGlySerL 134
|||||||||||||||:::||||||||||:::|||||
| GCTGAAGATGAGGATATCCAGGTTGGTGCCATGGCTGATCCTGGCATCTG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValPheTyrCysAlaLysValAlaSerValArgHisProLeuPheIleTr 117
                                                                                                                                                                                                                                                                                                             CAGACCAGCGCATGCCACACTACTCTCAGTCTTTGTCTTT.....GGGC
                                                                                                                                                                                                                                                                                                                                        eGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaGluP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        euLeuTyrValSerMetIleCysValPheHisSerLysTyrAlaGlyPhe 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTTTCTACTGTGCCAAGATTGCTACCATCCCTCACCCCACTCTTTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lileValIlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI 84
                                                                                                                                        qValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerP
                                                                                                                                                                                             SerLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerAr 216
                                                                                                                                                                                                                                                             heSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIlePhe 199
                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGTCTATGTAACTGTTACTACTTTCATCCATAGCAGAGAGACTTCAGAA 450
                                              LeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLeuValII
                                                                                                               GGAACCTAGCAGACATGCCCTCGTCAGTGCGATGCTCTCCATTCTGTCAT
                                                                                                                                                                                TCCCTGTGGAACCACAGCCGGCAGATGAGG...ACTATGGTGGGAACTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    782.00
3.218
81.271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200
                                                                                                                                                                                641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350
                                                                                                                                                                                                                                                                                                                544
                                                                                  249
                                                                                                                  691
                    266
```

```
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AF227140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_ro:AF227140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                     Align seg 1/1 to: AF227140
                                                                                                                                                                                             US-09-510-332-1 x AF227140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 ysLeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLysCysCys 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       792 TGGTATGTACCCCTCCTTACACTCGATTGTCTTAATTTTAGGAAACCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              742 CAAGGCCTCCACTTTGGAAGCAGAACCTTTGCATTCTGCTTATTGGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
eGlyIleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnProL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGATGGAAGGGCATATACTCTTCTTTTTTGGTTGTGATGGTGCAGTT
                                                                                                              MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF227140 1008 bp mRNA ROLL RATTLE norvegicus candidate taste receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF227140
AF227140.1 GI:7262626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-JAN-2000) NIDCR, Drive, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adler, E., Hoon, M.A., Mueller, K.L., and Zuker, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A novel family of mammalian taste receptors Cell 100 (6), 693-702 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zuker, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adler,E., Hoon,M.A., Mueller,K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus
                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1008)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 1008)
                                                                                                                                                                                                                                                                                                                                                                                         233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submission
                                                                                                                                                                                                                                                                                                                                                                                         a
                                                                                                                                                                                                                                                                                                                                                                                                                                     /Godon_start=1
/godon_start=1
/product="candidate taste receptor T2R1"
/protein_id="aar43913.1"
/protein_id="aar43913.1"
/db_xref="G::7262627"
/translation="MMEGHILFFFLVVMVQFVTGVLANGLIVVVHAIDLIMMKKMAPL
/translation="MMEGHILFFFLVVMVQFVTGVLANGLIVVVHAIDLIMMKKMAPL
/translation="MMEGHILFFFLVVMVQFVTGVLANGLIVVVHAIDLIMMKKMAPL
/translation="MMEGHILFFFLVVMVQFVTGVNTTFVFINESLATKPIFISLF
DLLLFCLATSRIILLFAULGIFAQUCLTFFFFTLAVLLITYSIMFXFGVMTTMVGTREYSG
PKNATQVGTGHATLLSVLVLGLTLPLFIFTVAVLLITYSIMFYFGLLVIGMYFSIHSIVLI
HAHISAMLSILSFLILYLSHYMVAVLISTQVLYLGSRTFVFCLLVIGMYFSIHSIVLI
HAHISAMLSILSFLILYLSHYMVAVLTSTQVLYLGSRTFVFCLLVIGMYFSIHSIVLI
                                                                                                                                                                                                                                                    767.00
3.156
81.271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="G protein-coupled receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             GNPKLKRNAKMFIVHCKCCHCTRAWVTSRSPRLSDLPVPPTHPSANKTSCSEACIMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1008
                                                                                                                                                                                                                                                                                                                                                                                         236
                                                                                                                                                                                                                                                                                                                                                                                         o
                                                                                                                                                         from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
Rodentia;
                                                                                                                                                                                                                                                      Percent
                                                                                                                                                                                                                                                                                                                                                                                         205
                                                                                                                                                           _
                                                                                                                                                                                                                                                                                                                                                                                         ω
                                                                                                                                                                                                                                                      Identity: 51.839
                                                                                                                                                           ţ
O:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH, Bldg. 10 Room 1N106, 10 Center
                                                                                                                                                                                                                                                                                                                                                                                         334 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chandrashekar, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chandrashekar, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T2R1 mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               841
                                                                                  50
                                                                                                                       17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ryba, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ryba, N.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murinae;
```

```
/ERSION
                     ACCESSION
                                                     DEFINITION
                                                                                      seq_documentation_block:
                                                                                                                          seq_name: gb_htg4:AC013470
                                                                                                                                                                                                                                                     266 eGlyIleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnProL 283
                                                                                                                                                                                                                                                                                                           742 CAAGTCCTCTACCTTGGAAGCAGAACCTTTGTATTCTGCTTACTGGTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34
                                                                                                                                                                                    ysLeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLysCysCys: 298
                                                                                                                                                                                                                                  TGGTATGTACCCCTCAATACACTCGATTGTCTTAATTTTAGGAAATCCTA 841
                                                                                                                                                                                                                                                                                                                                                                              heLeuIleLeuTyrPheSerHisCysMetIleLysValPheLeuSerSer
||||||||||||:::||||||
|TCCTCATCCTCTATCTCTCCCACTACATGGTGGCTGTTCTGATCTCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ValPheTyrCysAlaLysValAlaSerValArgHisProLeuPheIleTr
                                                                                                                                                                                                                                                                                                                                          LeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLeuValIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerLeuGlyArgH1sThrArgGlnMetArgAsnThrValAlaGlySerAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCACACTGCCGTTGTTCATCTTTACTGTTGCTGTTCTGCTCTTGATATAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euLeuTyrValSerMetIleCy9ValPheHi8SerLys...TyrAlaGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCTGAAACGAAATGCAAAAATGTTCATTGTCCATTGTAAGTGTTGT 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGTATAGCGGACATGCTCACATCAGTGCAATGCTGTCCATTCTATCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCCTGTGGAATTATAGCAGGCAGATGAGG...ACTATGGTAGGCACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIl 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGCTCTATGTAATTACTACTTTCATCCATAGCAGAGAGACTTCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  llleValIlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTTGATCATGTGGAAGAAAATGGCCCCGTTGGATCTGCTTCTATTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaGluP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATCCTTAAACCAATTTTTATA...AGCCTTTTTCCTAAAAATGCAACT..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTTCTACTGTGCCAAGATTGCTACCATTCCTCACCCACTCTTTCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGTCTTCATCATAAATGAACTGAGTCTTTGGTTTGCTACATGGCTCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGTCTATTCTCTTTGGTGAGACACACTTTATTTGAGGACAATATTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spLeuIIeLysHisArgLysMetAlaProLeuAspLeuLeuLeuSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . CAAGTCGGAACAGGGCATGCCACACTACTCTCAGTCCTGGTCCTTGGGC
           HOMO SAPIENS CHROMOSOME 7 Clone RP11-472F21, SEQUENCE, 18 unordered pieces. AC013470
 AC013470.6 GI:9211437
                                                 15-JUL-2000
WORKING DRAFT
                                                                                                                                                                                                                                                                                                           791
                                                                                                                                                                                                                                                                                                                                            266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                                                741
                                                                                                                                                                                                                                                                                                                                                                                                                   249
                                                                                                                                                                                                                                                                                                                                                                                                                                                       691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50
```

```
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (12-NOV-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Jul 15, 2000 this sequence version replaced g1:8954416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 180438) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 180438) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                           24146
32645
32745
41131
41231
49281
49381
60266
60366
60366
72487
72587
                                                                                                                                                                                                               10416
10516
17142
17242
                                                                                                                                                                                                    24046
                                                                                                                                                                                                                                                                                           1283
1383
2620
2720
                                                                                                                                                                                                               17241:
24045:
                                                                                                                                                                                                                                          10515:
17141:
                                                                                                                                                                                                                                                                                                          1382:
2619:
2719:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Center -----
             gap of
                                                     gap o
                                                                               gap of
                                                                                                                                                                                                                                                                                         contig of 1282 bp in length
gap of unknown length
contig of 1237 bp in length
gap of unknown length
contig of 1674 bp in length
                             conti
                                                                                                                                              gap or
                                                                                                                                                                                                gap
                                                                                                                     gap o
                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                   contig
                                                                                                                                 f unknown length
g of 8386 bp in
f unknown length
g of 8050 bp in
                                                                                                                                                                                   f unknown
g of 6626
f unknown
g of 6804
f unknown
f unknown
g of 8499
                                                                                                                                                                                                                                                                unknown
of 5922
                                                  of 12121 bp in length
unknown length
of 11857 bp in length
                                                                                         unknown length
of 10885 bp in length
unknown length
of 13378 bp in
                         unknown length of 10929 bp in
                                                                                                                                              bp in 1
length
                                                                                                                                                                                     dq
                                                                                                                                                                                                               bp in
                                                                                                                                                                                                                                       ur da
                                                                                                                                                                                                                                                                  ďď
                                                                                                                                                                          length
                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                   length
                                                                                                                                 length
                                                                                                                                                          length
                                                                                                                                                                                     length
                                                                                                                                                                                                              length
                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                  length
                          length
 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Louis
```

unknown

Length

```
FEATURES
                                                                                                                                                                   alignment_block:
US-09-510-332-1 x AC013470/rev
                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                  Quality:
Ratio:
Percent Similarity:
                                                                                                                                  Align seg 1/1 to reverse of: AC013470 from: 1
117069 AAATGGATTTCTTATCATTGTTAACTGTAATGAATTGATCAAACATAGAA 117020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                  23
                                                                                                 7 IleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheTh 23
                                                                  ATTCTTCATATTATCATGATGTCAGCAGAATTCTTCACAGGGATCACAGT
                             rAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArgL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133502
133602
151071
151171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109051
121519
121619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                            133602. .1510/v
/note="assembly_name:Contig29"
151171. .180438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_name:Contig12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="assembly_name:Contig18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="RP11-472F21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome="7"
                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig30"
32227 c 32003 g 56627 t
                                                                                                                                                                                                                                                                                                                                                                                                                                               vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="assembly_name:Contig17"
17242...24045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"assembly_name:Contig27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="assembly_name:Contig22"
                                                                                                                                                                                                                    438.50
2.118
68.771
                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_name:Contig28"
133602_ .151070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09051. .121518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="assembly_name:Contig26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="assembly_name:Contig21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121518: contig of 12468 bp in length 121618: gap of unknown length 133501: contig of 11883 bp in length 133601: gap of unknown length 151070: contig of 17469 bp in length 151170: gap of unknown length 180438: contig of 29268 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .180438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        te-"assembly_name:Contigl3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 1282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _e="assembly_name:Contig16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . .4393
.e="assembly_name:Contig14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e="assembly_name:Contig24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e="assembly_name:Contig25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e="assembly_name:Contig20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - "assembly_name:Contig19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .10415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .95472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .72486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .60265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .49280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .32644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .108950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .84443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /Qualifiers
                                                                                                                                                                                                                       Percent Identity:
                                                                                                                                                                                                                           33.555
                                                                                                                                       to: 180438
                                                                                                                                                                                                                                                                                                                                       1707 others
                                                                       117070
```

```
seq_documentation_block:
LOCUS AC005541 1:
                                                            seq_name: gb_pr2:AC005541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117019 AGCTAATGCCAATTCAAATCCTCTTAATGTGCATAGCGATGTCTAGATTT 116970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116869 TGTTTTTAGCTCTATCAGCCTATGGTTTGCCACTTGCCTTTCTGTATTT 116820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116969 GGTCTGCAGATGGTGATAATGGTACAAAGTTTTTTCTCTGTGTTCTTTTCC 116920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116669 GGAAGAGGATGCCCTCAGA.....AACACCACACACTAAAAA 116635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116534 CATCTCTTTACAAGCACACTCATCGGATGCAACATGGATCTCATGGCT 116485
                                                                                                                                                                                                                                                                                                                                                                   116390
                                                                                                                                                                                                                                                                                                                                                                                                                                                    116434 ACATTCTTTTGCTTCTTTATTTCTTAT.....TTTGCTGCCTTCATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116484 TTAGAAATGCCAACAGAAGCCCATATAAATGCATTAAAAACAGTGATA 116435
                                                                                                             116240 G 116240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACTCCTTTACGTCAAAATAATTTATGGTGCAGCAATGATGTTCCTTTGGA 116870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sMetArgIleSerLysLeuValProTrpMetIleLeuGlySerLeuLeu. 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePhe.. 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ysMetAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIle 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  euPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPhe 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     erArgValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeu 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ePheSerLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlyS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCATTAATATTTCCTCTAGCCATATTTGTGATGTGCACTTCTATGTTACT 116535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GluPheSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIl 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAGTAAAACAAAGATAAAGAAAATTAGTGAAGTGCTTCTTGTCAACTTG 116585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIleGlnL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTCTGTGAGCATTGCATCTGTGTGTCGAGGTAGATTACGCTAAAAATGT 116670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .TyrValSerMetIleCysValPheHisSerLys.TyrAlaGlyPheMe 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ysGluAspThrLeuAlaIleGlnIlePheSerPheVal.....Ala 181
                                                                                                                                                                                              GlyAsnProLysLeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLy 296
                                                                                                                                                                                                                                                                                AGGACATAATGGCAGCATATCCCTCTGGCCACTCGGTTATAATAATCTTG
                                                                                                                                                                                                                                                                                                       {\tt rSerLeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLeu}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerPheLeuIleLeuTyrPheSerHisCysMetIleLysValPheLeuSe 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116720
                                                                                                                                                                                                                                                                                                                                                                                                                    264
                                                                                                                                                                                                                                                                                                                                                                                                                                                             116391
                                                                                                                                                                                                                                                                                         116291
```

DEFINITION

AC005541 110626 bp DNA PRI Homo sapiens clone RG044L22, complete sequence.

14-JAN-1999

```
alignment_block:
US-09-510-332-1 x AC005541/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: AC005541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                4192 ACTCCTTTACGTCAAAATAATTTATGGTGCAGCAATGATGTTCCTTTGGA 4143
                                                                                                                                                                                                                                                                    4242 GGTCTGCAGATGGTGTTAATGGTACAAAGTTTTTTCTCTGTGTTCTTTCC 4193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4392 ATTCTTCATATTATCATGATGTCAGCAGAATTCTTCACAGGGATCACAGT 4343
                                                                                                                                                                                                                                                                                                                                                                                                                   4342 AAATGGATTTCTTATCATTGTTAACTGTAATGAATTGATCAAACATAGAA 4293
                                                                                                                                                                                                                                                                                                                                                                  40 ysMetAlaProLeuAspLeuLeuSerCysLeuAlaValSerArgIle 56
                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 rAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArgL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 IleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheTh 23
                                                                                                                         TACTGCCTCAAGATTTCAGGCTTCACTCAGTCCTGTTTTCTTTGGTTGAA
                                                                                       TyrCysAlaLysValAlaSerValArgHisProLeuPheIleTrpLeuLy 119
                                                                                                                                                                                                                                                                                                       PheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePhe. 72
                                                                                                                                                                                                                                  ......IleGluPheIleMetCysSerAlaAsnCysAlaIleLeuL
                                                                                                                                                                                                                                                                                                                                           AGCTAATGCCAATTCAAATCCTCTTAATGTGCATAGGGATGTCTAGATTT 4243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 110626)
Waterston,R.H.
Direct Submission
Submitted (14-JAN-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Jan 14, 1999 this sequence version replaced gi:3907453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (25-AUG-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
Eukaryota; Methazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 110626)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC005541
AC005541.1 GI:4156136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 110626)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            434.50
2.099
68.771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="RG044L22"
19647 c 20125 g 35478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .110626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110626
                                                     4043
                                                                                                                           4093
                                                                                                                                                                                                                                      86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Louis,
```

```
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pr4:AF227130
                                                                                                        TITLE
                                                                                                                                            AUTHORS
                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                   AUTHORS
                                                                                   JOURNAL
                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3513 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3563 AGTAATTCTAAGTTCCAACAATCATTTAGAAGAATTCTCTGCCTCAAAAA 3514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3857 GCATTAATATTTCCTCTAGCCATATTTGTGATGTGCACTTCTATGTTACT 3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4042 ATTCAGGATCCCAAAGTTAATACCTTGGCTGCTTCTGGGAAGCGTTCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296 s 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 erArgValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeu 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 GluPheSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIl 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGGACATAATGGCAGCATATCCCTCTGGCCACTCGGTTATAATAATCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SerPheLeuIleLeuTyrPheSerHisCysMetIleLysValPheLeuSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GlyAsnProLysLeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLy 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....VallleGlyIleTyrProSerGlyHisSerLeuIleLeuIleLeu 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAATATGACATTTAGTTTACCTTACAGAAGTCACCAGTTCTTTATGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rSerLeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLeu. 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACATTCTTTTGCTTCTTTATTTCTTAT....TTTGCTGCCTTCATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCTCTTTTACAAGCACACTCATCGGATGCAACATGGATCTCATGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ePheSerLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlyS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGTAAAACAAAGATAAAGAAAATTAGTGAAGTGCTTCTTGTCAACTTG 3858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ysGluAspThrLeuAlaIleGlnIlePheSerPheVal.....Ala 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAAGAGGATGCCCTCAGA......AACACCACACTAAAAA 3908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIleGlnL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCTGTGAGCATTGCATCTGTGTGTCGAGGTAGATTACGCTAAAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..TyrValSerMetIleCysValPheH1sSerLys.TyrAlaGlyPheMe
                                                                                                                                                                                                                                                                                                                                   human.
Homo sapiens
                                    Direct Submission
Submitted (21-JAN-2000) NIDCR, NIH,
Drive, Bethesda, MD 20892, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1. (bases 1 to 951)
                                                                                                                Adler,E., Hoon,M.A., Mueller,K.L., Chandrashekar,J., and Zuker,C.S.
                                                                                                                                                                                               Zuker, C.S.

A novel family of mammalian taste receptors Cell 100 (6), 693-702 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens candidate taste receptor T2R3
                                                                                                                                                                                                                                                         Adler,E., Hoon,M.A., Mueller,K.L., Chandrashekar,J.,
                                                                                                                                                                                                                                                                                                                                                                                                            AF227130.1
                                                                                                                                                               (bases 1 to 951)
∕organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                         GI:7262606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 951 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                          Bldg.
                                                                          10 Room 1N106, 10 Center
                                                                                                                                                                                                                                                                                                                                                                                                                                              gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3758
                                                                                                                                    Ryba, N.J.P.
                                                                                                                                                                                                                                                           Ryba, N.J. and
```

```
primer_bind
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-510-332-1 x AF227130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AF227130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer_bind CDS
                                                                      410
                                                                                                                                              360
                                                                                                                                                                               116
                                                                                                                                                                                                                   310
                                                                                                                                                                                                                                                     100
                                                                                                                                                                                                                                                                                                                                                              210
                                                                                                                                                                                                                                                                                                                                                                                                                                     172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
460
                                  139
                                                                                                        133
                                                                                                                                                                                                                                                                                          260 TTTCCTGGACATTTACAAACCATCTGAGCATTTGGCTTGCCACCTGTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 etAlaProLeuAspLeuLeuSerCysLeuAlaValSerArgIlePhe 57
                                                                                                                                                                                                                                                                                                                                                                                               74 uPheIleMetCysSerAlaAsnCysAlaIleLeuLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheIleGl 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArgLysM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGTTCCTGATTCTGTCTGGCACTCAGTTCACACTGGGAATTCTGGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGTTTCATTGAGTTGGTCAATGGTAGCAGCTGGTTCAAGACCAAGAGAA
                                                                                                                                                                eTrpLeuLysMetArgIleSerLysLeuValProTrpMetIleLeuGlyS:||||||||
                                                                                                                                                                                                                                        GlyValPheTyrCysAlaLysValAlaSerValArgHisProLeuPheIl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCTGTGTATTATCTTGACTGATAGT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAs
CTCTATTCTGTCTTTAGGGGAATTGAGGCCACCAGGAATGTGACTGAACA 509
                              MetIleCysValPheHisSerLysTyrAlaGlyPheMetValProTyrPh 155
                                                                                                                                             GGTGTCCTCTACTGCCTGAAAATCGCCAGTTTCTCTCACCCCACATTCCT
                                                                                                                                                                                                                                                                                                                                                                ATTCTCTCCCAACACACATGATTCAGGGATAATAATGCAAATTATTGATG
                                                                      CACTGCTCTTATCCTGTGGTAGTACCGCATCTCTGATCAATGAGTTTAAG
                                                                                                          erLeuLeuTyr........
                                                                                                                                                                                                                                                                                                                          .....pheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="candidate taste receptor T2R3"
/protein_id="AAP43903.1"
/protein_id="AAP43903.1"
/protein_id="AAP43903.1"
/db_xref="G1:7262607"
/db_xref="G1:7262607"
/translation="MMGLITEGVFLILSGTQFTLGILVNCFIELVNGSSWFKTKRMSLS
DFITTLALLRILLCIILTDSFLIERSPNTHDSGILMQIIDVSWTFFNHLSHWLATC
LGVLYCLKIASFSHPTFLWLKWRVSRVMVWMLLGALLLSGSTASLINEFKLYSVFRG
IEATRNVTEHFRKKRSBYZLIFVLGTLWYLPPLIVSLASYSLLIFSLGRHTROWLQNG
TSSRDPTTEAHKRAIRIILSFFFLFLLYFLAFLIASFGNFLPKTKMAKMIGEVMTMFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="candidate taste receptor T2R3" 933. .951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="G protein-coupled receptor; PCR-derived
similar to an interval in PAC AC004979"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="7q31.3-q32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405.00
2.166
59.744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAGHSFILILGNSKLKQTFVVMLRCESGHLKPGSKGPIFS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .951
221 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               â
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  209 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ţ.
                                                                                                        .....ValSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        313
8
36.422
                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTTAATAGA 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                          459
                                                                                                                                                                                   133
                                                                                                                                                                                                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                                    259
                                                                                                                                                                                                                                                                                                                                                                                                      86
                                                                                                                                                409
                                                                                                                                                                                                                       359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence;
```

```
REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AC004979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pr1:AC004979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                               COMMENT
                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                               AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                              JOURNAL
                                                             JOURNAL
                                                                                                                                             JOURNAL
                                                                                                                                                               TITLE
                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560 TG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189 IlePheLeuPheAlaValLeuLeuLeuIlePheSerLeuGlyArgHisTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 eLeuArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThrL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTATCCTGCTGGCCACTCATTTATCTCATTCTGGGGAACAGTAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rArgGlnMetArgAsnThrValAlaGlySerArgValProGlyArgGlyA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :::||||||
CTTCAGAAAGAAGAGAGTAGTTATCTGATCCATGTTCTTGGGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTGTCCCTGGCCTCCTACTCTTTGCTCATCTTCTCCCTGGGGAGGCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       \verb"euAlaIleGlnIlePheSerPheValAlaGluPheSerValProLeuLeu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LysGlnAsnAlaLysLysPheLeuLeuHisSerLysCys 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuTyrPheSerHisCysMetIleLysValPheLeuSerSerLeu...Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACGGCAGATGCTGCAAAATGGGACAAGCTCCAGAGATCCAACCACTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   leTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnProLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACCAAGATGGCTAAGATGATTGGCGAAGTAATGACAATG.....T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sPheHisIleArgArgPheIlePheLeuPhePheIleLeuValIleGlyI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTTACTTTCTTGCTTTCTTAATTGCATCATTTGGTAATTTCCTACCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     laProIleSerAlaLeuLeuSerIleLeuSerPhe.....LeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGCAGACA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens PAC
              Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 6
On Jan 13, 1999 this sequence version replaced g1:3264780.
                                                                                                            Waterston,R.
Direct Submission
Submitted (13-JAN-1999) Department of Genetics,
University, 4444 Forest Park Avenue, St. Louis,
4 (bases 1 to 82419)
                                                                                                                                                                                                            Submitted (12-JUN-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 82419)
Du,H., Duckels,G. and Kock,J.
The sequence of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC004979
AC004979.1 GI:4153864
                                                                                                Waterston, R
                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                  Waterston, R.H.
                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                              (bases 1 to 82419)
                                                                                                                                                                                                                                                                                             (bases 1 to 82419)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82419
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .TTTGTAGTGATGCTCCGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....TGGTACCTGCCTCCCTTAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RP5-1154E9
University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                                                                                                                                  PAC clone RP5-1154E9
                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from 7q31.3-q32,
                                                                                                                                                                                                                                                                                                                                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251
                                                                                                                                   Washington
Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete
                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
                                                  63108,
                                                                                                                                                                                                                                       Louis,
```

```
misc_feature
                                                                          repeat_region
                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7, send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The clone sequenced to the left is RP5-894A10, 200 bp overlap; the clone sequenced to the right is unknown. Actual start of this clone is at base position 103168 of RP5-894A10; actual end is at 82419 of RP5-1154E9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one male donor.

The clone may be obtained either from Genome Systems, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Toannou et al., Nature Genetics 6:84-9 (1994). The library is from the composition of the composition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VECTOR: PCYPAC2
NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAPPING INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://genome.wustl.edu/gsc
Contact: saplens@watson.wustl.edu
----- Summary Statistics
Center project name: H_DJ1154E09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="MER1_type"
801, .1104
                                                                                /rpt_family-"Alu"
3226. .3272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="7q31.3-q32"
/clone="RP5-1154E9"
/clone_lib="RPCI-5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence may not represent the entire insert of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_tamily-"Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                             rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                          rpt_family="Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family-"Alu"
                                          _family="AT_rich"
                                                                                                                                                                     _family-"MER2_type"
                                                                                                                                                                                                                                  _famil
                                                                                                                                                                                                                                                                   .1865
                                                                                                                                                                                                                                  y≖"MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                 y="MER1_type"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                repeat_region
                                                                                             repeat_region
                                                                                                                                                                                                               repeat_region
                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                   /rpt_family="AT_rich"
23385. .29503
rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GI:435384"
3587. .3874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3365. .3878

/note="match to EST AA649071 (NID:g2575500) ns42h02.s1"

3498. .3878

/note="match to EST AI031578 (NID:g3249790) ow06e12.x1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match to EST C15294 (NID:g1570001)*
3365. .3878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to EST D57847 (NID:g964469)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt_family="Retroviral"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_fam:
                                                                                                                           _fami
                                                                                                                                                                                     _family="MaLR"
                                                                                                                                                                                                                                                  fami
                                                                                                                                                                                                                                                                                                                                                                          _fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _fami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _family-"Alu"
                                                                                                                                                                                                                                                                                                                fami
                                                                                                                                                                                                                                                                                                                                                                                                                                     fam:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .tami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family-"MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      family-"MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family-"Alu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family-"(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family-"MER73-group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _family=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         family="Retroviral"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family-"MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family-"MaLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family-"AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                family-"L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family-"L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        famil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          family-"MaLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family-"MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4293
                                                                                                                                                                                                                                                                                                                                                                                                           .21896
                                                                                                                                                                                                                     22865
                                                                                                                           ly-"MIR"
                                                                                                                                                                                                                                                                                                   Ly-"L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ly-"Retroviral"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ly-"L2"
                                                                                                                                                                                                                                            Ly-"MIR"
                                                                                                                                                                                                                                                                                                                                                                       ly-"L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ly-"Retroviral"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y="Retroviral"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         y="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /- "purine-rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     γ-"MalR"
                                                                                                                                                                                                                                                                                                                                                                                                                                 "(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "MaLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "AT_rich"
```

FEATURES

source

```
Page
```

```
alignment_block:
US-09-510-332-1 x AC004979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AC004979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17647
                                                                                                                                                                               17935 CTGGCTCAAGTGGAGAGTTTCTAGGGTGATGGTATGGATGCTGTTGGGTG 1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17747
                                      18035 CTCTATTCTGTCTTTAGGGGAATTGAGGCCACCAGGAATGTGACTGAACA 18084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                  74
                                                                                                                                             133 erLeuLeuTyr......valSer 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 nGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArgLysM 41
155 eLeuArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThrL 172
                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 IleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAs 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGTTCCTGATTCTGTCTGGCACTCAGTTCACACTGGGAATTCTGGTCAA 17646
                                                                                                                                                                                                                                                        GGTGTCCTCTACTGCCTGAAAATCGCCAGTTTCTCTCACCCCACATTCCT 17934
                                                                                                                                                                                                                                                                           GlyValPheTyrCysAlaLysValAlaSerValArgHisProLeuPheIl 116
                                                                                                                                                                                                                                                                                                                             TTTCCTGGACATTTACAAACCATCTGAGCATTTGGCTTGCCACCTGTCTT 17884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGCTGTGTATTATCTTGACTGATAGT.....TTTTTAATAGA 17784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      etAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePhe 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGITICATIGAGITGGTCAAIGGTAGCAGCTGGTICAAGACCAAGAGAA 17696
                                                                                                                                                                                                              eTrpLeuLysMetArgIleSerLysLeuValProTrpMetIleLeuGlyS 133
                                                                                                                                                                                                                                                                                                                                                           ATTCTCTCCCAACACACATGATTCAGGGATAATAATGCAAATTATTGATG 17834
                                                                                                                                                                                                                                                                                                                                                                                                                                    uPheIleMetCysSerAlaAsnCysAlaIleLeuLeu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheIleGl 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTCTTTGTCTGACTTCATCATCACCACCCTGGCACTCTTGAGGATCATT 17746
                                                                    MetIleCysValPheHisSerLysTyrAlaGlyPheMetValProTyrPh 155
                                                                                                           CACTGCTCTTATCCTGTGGTAGTACCGCATCTCTGATCAATGAGTTTAAG 18034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_
35173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="AT_rich" 34523. .34757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="Alu" 34209. .34235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_37719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="MIR"
36544. .36581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             405.00
2.166
59.744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="MIR"
38203. .38257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family="(TAGA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family="MaLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  family="(GGGA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .38372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .33635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .37867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .36050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .35170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 313
Gaps: 8
Percent Identity: 36.422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 82419
                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                                            86
```

```
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_pr4:AF227134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18208
                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18158 GTGTCCCTGGCCTCCTACTCTTTGCTCATCTTCTCCCTGGGGAGGCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18085 CTTCAGAAAGAAGAGGAGTGAGTATTATCTGATCCATGTTCTTGGGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18258 CCCACAAGAGGGCCATCAGAATCATCCTTTCTTCTTCTTCTTTA 18307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18449 AAGCAGACA.....TTTGTAGTGATGCTCCGGTGT 18478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 IlePheLeuPheAlaValLeuLeuLeuIlePheSerLeuGlyArgHisTh 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 euAlaIleGlnIlePheSerPheValAlaGluPheSerValProLeuLeu 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251
                                                                                                         primer_bind
CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rArgGlnMetArgAsnThrValAlaGlySerArgValProGlyArgGlyA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sPheHisIleArgArgPheIlePheLeuPhePheIleLeuValIleGlyI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTTACTTTCTTGCTTTCTTAATTGCATCATTTGGTAATTTCCTACCAAA 18357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACGGCAGATGCTGCAAAATGGGACAAGCTCCAGAGATCCAACCACTGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuTyrPheSerHisCysMetIleLysValPheLeuSerSerLeu...Ly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laProIleSerAlaLeuLeuSerIleLeuSerPhe.....LeuIle 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysGlnAsnAlaLysLysPheLeuLeuHisSerLysCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AACCAAGATGGCTAAGATGATTGGCGAAGTAATGACAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens candidate taste receptor T2R8 gene, AF227134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF227134.1 GI:7262614
                                                                                                                                                                                                                                                                                                                                                                             A novel family of mammalian taste receptors CC11 100 (6), 693-702 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                      Submitted (21-JAN-2000) NIDCR, Drive, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                          Adler, E., Hoon, M.A., Mueller, K.L., and Zuker, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                   adler,E., Hoon,M.A., Mueller,K.L., Chandrashekar,J.,
zuker,C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                            Direct Submission
                                                                                                                                                                                                                                                                                                                                              (bases 1 to 930)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 930)
                                                                   /note="G protein-coupled receptor; PCR-derived similar to an interval in BAC AC006518"
                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/codon_start=1
/product="candidate taste receptor T2R8"
/protein_ida"MAF43907.1"
/db_xref="G1:7262615"
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                            'map="12p13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....TGGTACCTGCCTCCCTTAATT 18157
                                                                                                                                                                                                                                                                           HIN,
                                                                                                                                                                                                                                                                                                                                 Chandrashekar, J.,
                                                                                                                                                                                                                                                                           в1dg. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . . . . . . . . . . . . T
                                                                                                                                                                                                                                                                               Room 1N106, 10 Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                              Ryba, N.J. and
                                                                                                                                                                                                                                                                                                                                   Ryba, N.J.P.
                                                                                                sequence;
```

```
allgnment_block:
US-09-510-332-1 x AF227134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer_bind
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AF227134
                                                                           165
182 GluPheSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIl 198
                                                                                                                                                                                                               143
                                                                                                                                                                                                                                                 419
                                                                                                                                                                                                                                                                                    135
                                                                                                                                                                                                                                                                                                                    369
                                                                                                                                                                                                                                                                                                                                                     119
                                                                                                                                                                                                                                                                                                                                                                                                                        103
                                                                                                                                                                                                                                                                                                                                                                                                                                                   269 CATTTGCCAACTACTTAAATATGTGGATTACCACCTGCCTTAATGTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         122 TTTCCACAGTTGACTACATCCTTACCAATTTAGTTATCGCCAGAATTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 uPheIleMetCysSerAlaAsnCysAlaIleLeuLeu......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 etAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                   aGlyPheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaT
                                                                                                                                                                                                                                                                                                                                          sMetArgIleSerLysLeuValProTrpMetIleLeuGlySerLeu.... 134
                                                                                                                                                                                                                                                                                                                                                                                                    TyrCysAlaLysValAlaSerValArgHisProLeuPheIleTrpLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..PheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPhe 102
                                                                    hrIleGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAla
                                                                                                        TGTGAGTAAAATACCATACTTT....
                                                                                                                                                                       AGGTTTCATGCAATTGCCAAACATAAAAGAAACATTACTGAAATGTTCCA 518
                                                                                                                                                                                                      ...PheHisSer.....LysTyrAl
                                                                                                                                                                                                                                            TTTCCTTGTTGGTCAGCCTTATAGCAGCAATAGTACTGAGTTGTGATTAT
                                                                                                                                                                                                                                                                                                             GTGGAAAATTGATATGGTGGTGCACTGGATCCTGCTGGGATGCTTTGCCA
                                                                                                                                                                                                                                                                                                                                                                                TATTTTCTGAAGATAGCCAGTTCCTCTCATCCACTTTTTCTCTGGCTGAA
                                                                                                                                                                                                                                                                         .....LeuTyrValSerMetIleCysVal..........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGATGTTTATACAAAAATAAACAACAGATAGTCATTTTTACCTTCTGGA 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuGlnLeuPheTlePheTyrValAsnValIleValIlePhePheIleGl 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nGlyIleIleValValAsnGlyIleAspLeuIleLysHisArgLysM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTG...ATCAGTGTAATGGTTGTAAATGGCATTGTAATAGTACTGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGATACATTGCACTAGTCAACTGGATTGACTGGATTAAGAAGAAAAAGA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                    ....GAACCCTTGACTCTTTTAACCTGTTTGCAATT....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         376.00
2.000
58.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="candidate taste receptor T2R8" 907. .930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MFSPADNIFIILITGEFILGILGNGYIALVNWIDWIKKKKISTV DYILTMUVIARICLISYMVVNGIVIVUMDDVYKKKQQIVIFTEWTFANYLNMWITTG LNVFYFLKIASSSHPLFLWLKWKIDMVVHWILLGCFAISLLVSLIAAIVLSCDYRFHA IAKHKRNITEMFHVFKLEWLFWLFWLFWLFVISSISFFLLVRSLWRHTKQIKLY ATGSRDPSTEVHVRAIKTMTSFIFFFFLYYISSILMTFSYLMTKYKLAVEFGEIAAIL YPLGISLIVIVLNKLRQTFVRMLTCRKIACMI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 320
Gaps: 10
Percent Identity: 31.562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ç
o:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ۲
                                                                                                                                                                                                                                                                              142
                                                                                                                                                                                                                                                                                                               418
                                                                                                                                                                                                                                                                                                                                                                                                                  119
                                                                                                                                                                                                                                                                                                                                                                                                                                                   318
                                    573
                                                                      181
                                                                                                     540
                                                                                                                                         165
                                                                                                                                                                                                          148
                                                                                                                                                                                                                                            468
                                                                                                                                                                                                                                                                                                                                                                                  368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24
```

```
JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
· ORGANISM
                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_pr4:AF227133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rocus
                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                     primer_bind CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HisSerLeuIleLeuIleLeuGlyAsnProLysLeuLysGlnAsnAlaLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAGAGACCCCAGCACAGAAGTTCATGTGAGAGCCATTAAAACTATGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGAATGCTG 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sLysPheLeu 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACTCACTTATTTTAATTGTTTTAAATAATAAACTGAGGCAGACATTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTTAGCTGTGGAGTTTGGAGAGATTGCAGCAATTCTCTACCCCTTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rSerLeuLysPheHisIleArgArgPheIlePheLeu......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerPheLeuIleLeuTyrPheSerHisCysMetIleLysValPheLeuSe 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ......PhePheIleLeuValIleGlyIleTyrProSerGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTATT....TTGATGACCTTTAGCTATCTTATGACAAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCATTTATCTTCTTTTTTTCCTATAC.........TATATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erargValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGATCTTTATGGAGACATACCAAGCAAATAAAACTCTATGCTACCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·····GTCCCATTTATTGTGTCACTGATATCATTTTTCCTTTTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 957)
Adler,E., Hoon,M.A., Mueller,K.L., Chandrashekar,J., Zuker,C.S.
                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 957)
Adler,E., Hoon,M.A., Mueller,K.L.,
and Zuker,C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cell
                                                                                                                                                                                                                                                                                                                                          Submitted (21-JAN-2000) NIDCR, Drive, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF227133.1 GI:7262612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2022257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 (6),
                                                                                                                                                                                                                                                                                                                                                                                                                                                              family of mammalian taste receptors 0 (6), 693-702 (2000)
/translation="madkvQTTLLFLAVGEFSVGILGNAFIGLVNCMDWVKKKIASI
DILITSALISRICLLCVILLDCFILVLIPDVYATGKEMRIIDEFMTLTMHLSIMFATC
LSITYTEFKIANEFEHPLE-HAMKWRIBORVISWILLDGCVPLSVEFISLPATENLNADFRFCV
KAKRKTNLTWSCRVNKTQHASTKLFLNLATLLDFCVCLMSFFLLILSLIRHIRRNQLS
ATGCRDPSTEAHVRALKAVISFLLLFIAYYLSFLIATSSYFMPETELAVIFGESIALI

    .957
/note="G protein-coupled receptor; PCR-derived similar to an interval in BAC AC006518"

                                                                                            /product="candidate taste receptor T2R7"
/protein_id="AAF43906.1"
/db_xref="GI:7262613"
                                                                                                                                                                                                                                  /chromosome="12"
/map="12p13"
                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxbn:9606"
                                                                                                                                                                                                                                                                                                                         ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               đđ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         taste receptor T2R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                          , HIN
                                                                                                                                                                                                                                                                                                                                                                                                            Chandrashekar, J.,
                                                                                                                                                                                                                                                                                                                                                          Bldg. 10 Room 1N106,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-2000
complete cds
                                                                                                                                                                                                                                                                                                                                                                                                            Ryba, N.J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ryba, N.J.
                                                                                                                                                                               sequence;
                                                                                                                                                                                                                                                                                                                                                          10 Center
```

```
primer_bind
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-510-332-1 x AF227133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                       384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284
                                                                                                                                                                                                                                                                                                                                      422
                                                                                                                                                                                                                                                                                                                                                        141 ysvalpheHisSerLysTyrAla......Gly 149
                                                                                                                                                                                                                                                                                                                                                                                                                                         124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522
                                                                                                                                                                                                                                  166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 ATTGGTAAACTGCATGGACTGGGTCAAGAAGAGGAAAATTGCCTCCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 LeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIleIleVa
                              216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lValValAsnGlyIleAspLeuIleLysHisArgLysMetAlaProLeuA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                   sLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSerMetIleC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IlePheTyrValAsnValIleValIlePhePheIleGluPheIleMetCy 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTTAATCCTCACAAGTCTGGCCATATCCAGAATTTGTCTATTGTGCGTA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              spLeuLeuLeuSerCysLeuAlaValSerArgIlePheLeuGlnLeuPhe 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTAATTTCTTTCACCCACTTTTCCTCTGGATGAAGTGGAGAATTGACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AlaSerValArgHisProLeuPheIleTrpLeuLySMetArgIleSerLy 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTAAAGAAATGAGAATCATTGACTTCTTCTGGACACTAACCAATCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sSerAlaAsnCysAlaIleLeuLeuPheIle......AsnGluL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATACTATTAGATTGTTTATATTGGTGCTATATCCAGATGTCTATGCCAC
                                                                                                                                                  heSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIlePhe 199
                                                                                                                                                                                                                               eGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaGluP 183
                                                                                                                                                                                                                                                                                               PheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIl 166
                                                                                                                                                                                                                                                                                                                                     CTGTGTTTATTAGCCTTCCAGCCACTGAGAATTTGAACGCTGATTTCAGG 471
                                                                                                                                                                                                                                                                                                                                                                                                     GGTGATTTCCTGGATTCTACTGGGGTGCGTG......GTTCTCT 421
                                                                                                                                                                                                  AAATAAAACTCAACATGCTTCTACCAAGTTATTTCTCAACCTGGCAACGC
                                                                                                                                                                                                                                                                   TTTTGTGTGAAGGCAAAGAGGAAAACAAACTTAACTTGGAGTTGCAGAGT 521
                          gValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerP 233
                                                                                            SerLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerAr
                                                                                                                              TG...CTCCCCTTTTGTGTGTGCCTAATGTCCTTTTTCCTCTTGATCCTC
AGACCCCAGCACAGAAGCCCATGTGAGAGCCCCTGAAAGCTGTCATTTCCT
                                                                  TCCCTGCGGAGACATATCAGGCGAATGCAGCTCAGTGCCACAGGGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: AF227133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="candidate taste receptor T2R7" 936. .957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376.00
1.979
64.626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YPSSHSFILILGNNKLRHASLKVIWKVMSILKGRKFQQHKQI" <1. .>957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bercent Identity: 32.653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233
                                                                     668
                                                                                                       216
                                                                                                                                         618
                                                                                                                                                                                                        571
```

```
seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 heLeuIleLeuTyrPheSerHisCysMetIleLysValPheLeuSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         869 ATAAATTAAGACATGCATCTCTAAAGGTGATT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
Dugan-Rocha, S., Durbin, K. J., Fernandez, C., Ferraguto, D.,
Dugan-Rocha, S., Durbin, K. J., Fernandez, C., Ferraguto, D.,
Everyara, W., Harris, K., Ganesh, R., Gorrell, J.H., Gorrell, J.L.,
Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,
Holloway, C., Hosak, H., Jackson, L. E., Jackson, L., Jia, Y., Jones, M.,
Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Kelly, S., Kondejewski, N., Logan, O., Lozado, R. J., Lu, J.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R. J., Lu, J.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R. J., Lu, J.,
Lucier, R., Martin, R., Martinez, C., McLeod, M. P., Mei, G., Morgan, M.,
Morris, S., Nash, S., Nelson, A., Nguyen, S.,
Morris, S., Nash, S., Nelson, A., Nguyen, S.,
Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L. L.,
Oswal, G., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L. L.,
Oswal, G., Parish, B., Paxton, S., Payton, B., Samps, A., Sucgang, R.,
Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R.,
Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wahbah, M.,
Watlington, S., Weinstock, G., Weinstock, I. R., Williamson, A.,
Watlington, S., Weinstock, G., Weinstock, I. R., Williamson, D., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roLysLeuLysGlnAsnAlaLysLysPheLeu 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eGly...IleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnP 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTACTTTATGCCAGAGACGGAATTAGCTGTGATTTTTGGTGAGTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLeuValIl 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_htg5:AC016145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny, D.M., Adams, C., Bailey, M., Buroks, A., Buhay, C., Bunac, C., Bodota, B., Bouck, J., Bowle, S., Brooks, A., Buhay, C., Chen, Z., Cox, C., Cox, C., Chen, Z., Chen, Z., Cox, C., Chen, Z., Cox, C., Chen, Z., Chen, Z., Cox, C., Chen, Z., Chen, Z.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome 20 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 16253)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Worley,K.C.
Direct Submission
Submitted (23-NOV-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Daylor Plaza, Houston, TX 77030, USA On Aug 26, 2000 this sequence version replaced gi:9719589.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC016145.10 GI:9929535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC016145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 162553)
sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 12% of reads
Chemistry: Dye-terminator Big Dye: 86% of reads
Chemistry: Dyerterminator Big Dye: 86% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 129880 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                        Center project name: HMQY
Center clone name: RP13-81N3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162553

    Genome Center

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A HTG clone RP13-81N3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-2000
WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                818
```

```
alignment_block:
US-09-510-332-1 x AC016145/rev
                                                                                             alignment_scores:
                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                               FEATURES
                                                    Percent Similarity:
                                                                                                                                                                                                                                 source
                                                                  Quality:
Ratio:
                                                                                                                                                         50057 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "vorking draft" sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Consensus quality: 145651 bases at least Q30 Consensus quality: 151922 bases at least Q20 Estimated insert size: 154982; sum-of-contigs estimation Estimated insert size: 135000; agarose-fp estimation Quality coverage: 3.9x in Q20 bases; agarose-fp estimation Quality coverage: 3.4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28949
29049
47982
48082
                                                  376.00
1.979
64.626
                                                                                                                                                   /clone="RP13-81N3"
30129 c 29217 g
                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
                                                                                                                                                                                                                                          Location,
                                                                                                                                                                                                                                                       .60794: gap of unknown 62553: contig of 1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28948: contig
29048: gap of
                                                                                                                                                                                                                                            /Qualifiers
                                                 Percent Identity: 32.653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of contig gap of contig gap of contig gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of contig gap of contig
                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
contig
                                                                                                                                                                                                                                                                                                                 conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                           conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                            g of 6080 bp in length tunknown length g of 4402 bp in length funknown length g of 3400 bp in length funknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g of 5247 bp in 1
f unknown length
g of 10973 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       f unknown length
g of 10261 bp in
f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
of 9720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 28948 bp in unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown length
of 17351 bp in
                                                                                                                                                                                                                                                                                     of 1098
                                                                                                                                                                                                                                                                                                                 o
H
                                                                                                                                                                                                                                                                                                                               unknown
                                                                                                                                                                                                                                                                                                                                              of 1760
                                                                                                                                                                                                                                                                                                                                                                                                                                   of 410:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 9002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 8754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 10877 bp
                                                                                                                                                      51223 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18933 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
bp in
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
bp in l
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
bp in
                                                                                                                                                                                                                                                                                                                                                          bp in length
                                                                                                                                                                                                                                                        đđ
                                                                                                                                                                                                                                                                                  dq
                                                                                                                                                                                                                                                                                                               dq
                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                     ģ
                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                      leng
                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                   1927 others
                                                                                                                                                                                                                                                        1n
                                                                                                                                                                                                                                                                               in length
                                                                                                                                                                                                                                                                                                                                          in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                       in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in length
                                                                            294
                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
```

```
Align seg 1/1
                                                                                                                                                                  57732
                                                                                                                                                                                                                                                                                                                                               57832 AGACCCCAGCACAGAAGCCCCATGTGAGAGCCCCTGAAAGCTGTCATTTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                  57882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57979 AAATAAAACTCAACATGCTTCTACCAAGTTATTTCTCAACCTGGCAACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58267 TGGTAAAGAAATGAGAATCATTGACTTCTTCTGGACACTAACCAATCATT 58218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58317 ATACTATTAGATTGTTTTATATTGGTGCTATATCCAGATGTCTATGCCAC 58268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58417 ATTGGTAAACTGCATGGACTGGGTCAAGAAGAGGAAAATTGCCTCCATTG 58368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 roLysLeuLysGlnAsnAlaLysLysPheLeu 292
                                                                                                                                                                                                                                                                                                          233
                                                                                                                                                                                                                                                                                                                                                                                                     216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 heSerValProLeuLleuPheLeuPheAlaValLeuLeuLeuIlePhe 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 ysValPheHisSerLysTyrAla......Gly 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45 spLeuLeuSerCysLeuAlaValSerArgIlePheLeuGlnLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 LeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIleIleVa 28
                                                                                      eGly...IleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnp
                                                                                                                                                           AGCTACTTTATGCCAGAGACGGAATTAGCTGTGATTTTTGGTGAGTCCAT
                                                                  AGCTCTAATCTACCCCTCAAGTCATTCATTTATCCTAATACTGGGGAACA 57633
                                                                                                                                                                                                       LeuLysPheHisIleArgArgPheIlePheLeuPhePheIleLeuValIl 266
                                                                                                                                                                                                                                               TCCTTCTCCTCTTATTGCCTACTATTGTCCTTTCTCATTGCCACCTCC
                                                                                                                                                                                                                                                                                                heLeuIleLeuTyrPheSerHisCysMetIleLysValPheLeuSerSer
                                                                                                                                                                                                                                                                                                                                                                                                                                          TCCCTGCGGAGACATATCAGGCGAATGCAGCTCAGTGCCACAGGGTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SerLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGATTTCCTGGATTCTACTGGGGTGCGTG......GTTCTCT 58080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTAATTTCTTTCACCCACTTTTCCTCTGGATGAAGTGGAGAATTGACAG 58118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysVal 107
                                                                                                                                                                                                                                                                                                                                                                                            gValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TG...CTCCCCTTTTGTGTGTGCCTAATGTCCTTTTTCCTCTTGATCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAlaGluP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTGTGTGAAGGCAAAGAGGAAAACAAACTTAACTTGGAGTTGCAGAGT 57980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIl 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTGTTTATTAGCCTTCCAGCCACTGAGAATTTGAACGCTGATTTCAGG 58030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSerMetIleC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AlaSerValArgHisProLeuPheIleTrpLeuLysMetArgIleSerLy 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAGTATCTGGTTTGCAACCTGCCTCAGCATTTACTATTTCTTCAAGATA 58168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sSerAlaAsnCysAlaIleLeuLeuPheIle......AsnGluL 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTTAATCCTCACAAGTCTGGCCATATCCAGAATTTGTCTATTGTGCGTA 58318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IlePheTyrValAsnValIleValIlePhePheIleGluPheIleMetCy 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lValValAsnGlyIleAspLeuTleLysHisArgLysMetAlaProLeuA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to reverse of: AC016145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162553
                                                                                                               282
                                                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                                                                                                              233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183
                                                                                                                                                                                                                                                      57733
                                                                                                                                                           57683
                                                                                                                                                                                                                                                                                                                                                  57783
                                                                                                                                                                                                                                                                                                                                                                                                                                             57833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
```

```
57632 ATAAATTAAGACATGCATCTCTAAAGGTGATT 57601
gb_pr2:AC006518
```

seq_documentation_block: LOCUS AC006518 1 DEFINITION VERSION ACCESSION AC006518 173735 bp DNA PRI 01-MAY-1999 Homo sapiens 12p13 BAC RPCI11-144023 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

AC006518.17 GI:4713939 HTG.

SOURCE ORGANISM KEYWORDS Homo sapiens

REFERENCE AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 173735)

Muzny,D., Arenson,A.D., Bouck,J., Bunac,C., Chen,Z., Ding,Y., Dugan,S., Durbin,J., Forcum,J., Garcia,C., Gorrell,J.H., Correll,L.L., Hernandez,J., Issar,A., Jackson,L., Kneitz,S., Kondejewski,N., Lau,S., Leal,B., Lee,E., Lichtarge,O., Liu,W., Logan,O., Lu,J., Marondel,I., Martinez,C., Merscher,S., Miller,A., Montgomery,K., Oswal,G., Pampell,L.R., Parish,B.J., Perez,L., Mashid,N.D., Rives,C., Scherer,S.E., Shen,H., Shim,C., Simon,M., Vo,Q., Williamson,A., Worley,K.C., Xhang,A.M., Yang,R., Yu,W., Zhou,X., Kucherlapati;R., Nelson,D. and Gibbs,R.A.

TITLE
JOURNAL
REFERENCE
AUTHORS TITLE

REFERENCE JOURNAL AUTHORS Worley K.C.

Morley K.C.

Direct Submission
Submitted (05-FEB-1999) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 173735)
Worley K. Worley, K.C. Direct Submission

REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

gc-help@bcm.tmc.edu

JOURNAL TITLE

Submitted (29-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 173735)
Worley.K.C.
Direct Submission Submitted (01-MAY-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Apr 29, 1999 this sequence version replaced gi:4589934. INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the a region does not meet this standard,

annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.

QUALSTAT-REPORT-----

5 10 15 20 25 Phrap Value Range	1000 900 900 800 100 100 100 100 100 100 1	Distribution of Quality < 40 Bases	Position Original+Context 31176 gtgggttgg(n)agaggggag 31177 tggggttgggn(a)gagggggag 104155 gagtttcact(n)tgttgtcctc	Contig length: Phrap values in estimate: Average error rate (BCM-Phrap estimate): Fraction of Phrap values less than 40: Number of consensus changing edits: Number of N's in consensus:
30 35 40 inge	*****	Bases	Edited+Context gtgggtggg(g)gagggggag tggggtggg(g)gagggggag gagtttcact(c)tgttgtcctc	173735 167393 0.000263256 0.0395058 3

repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region	repeat_region				source	Version:	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
/ipc_ramriy= Purific complement(1395413975)	1335: 15: 15: 15: 15: 15: 15: 15: 15: 15: 1	12968 . 13198 /rnt family="MTR"	<pre>complement(12644: .12693) /rnt family="L1MA4"</pre>	complement(1223312365) /rpt_family="FLAM_C"	1165211865 /rpt_family="MER80"	<pre>complement(1020910241) /rpt_family="AT_rich"</pre>	68336962 /rpt_family="AluSg/x"	<pre>complement(29853277) /rpt_family="Alusp"</pre>	18731957 /rpt_family="MER53"	/chromosome="12pl3"	/db_xref="taxon:9606"	/organism="Homo sapiens"	1173735	1.01 qxfo. Location/Qualifiers	

```
allgnment_scores:
Quality: :
Ratio:
Percent Similarity: 5
                                                                                                             alignment_block:
US-09-510-332-1 x AC006518/rev
                                                                       Align seg 1/1 to reverse of: AC006518 from: 1 to: 173735
repeat_region
                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                        complement(29508. .2959)
/rpt_family="(TAAA)n"
complement(29500. .29858)
/rpt_family="Alux"
complement(30569. .30398)
/rpt_family="AT_rich"
31146. .31316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="AluJo"

complement(28088. 28123)

/rpt_family="(A)n"

complement(28124. 28214)

/rpt_family="(TA)n"

28277. 28381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="L1PA16"
/rpt_family="11PA16"
/rpt_family="Arrich"
complement(1958. . 20023)
/rpt_family="11PB2"
/rpt_family="11PB2"
/rpt_family="11NA5A"
/rpt_family="11NA5A"
/rpt_family="Arrich"
                                                                                                                                                               376.00
2.000
58.750
                                                                                                                                                                                                                                                 /rpt_family="AluJo"
complement(32384. .33480)
/rpt_family="LIMA5"
                                                                                                                                                                                                                                                                                                        /rpt_family="L1PA2" 31857. .32070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="L1M4"
28925, 20060
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="MLT1A1"
29201. .29267
/rpt_family="Alus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family-"L1M4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family-"L1M4"
14652. .14742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="AT_rich"
14232 .14649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'rpt_family="L1MA4A"
18679. .18844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family-"L1MB5"
18072. .18210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="L1MB5"
16238. .16272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="(TA)n"
15287. .15421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pt_family-"L1M4"
269. .27511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _family="U2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family="MER46"
3. .28087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family-"L1M4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _family="L2"
                                                                                                                                                           Length: 320
Gaps: 10
Percent Identity: 31.562
```

24 5820	nGlyIleIleValValValAsnGlyIleAspLeuIleLysH1sArgLysM 4	1 771
41 5770	etAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePhe 5 ::::: :::	7 721
58 5720	LeuGlnLeuPheIlePheTyrValASnValIleValIlePhePheIleG1 7	674
74 5673	uPheIleMetCysSeralaAsnCysAlaIleLeuLeu	6 624
87 5623	PheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPhe 1	02 574
103 5573	LysValAlaSerValArgHisProLeuPheIleTrpLeuLy 1 :::	.19
119 5523	ySerLeu 1 ::: ATGCTTTGCCA 5	34
135 5473		424
143 5423		374
148 5373	/sPhePheSerGlnAsnAlaT 16	5 5
165	rPheValAla 18	_
182 5318	uPheSerValProLeuLeuIlePheLeuPheAlaValLeuLeuIl 19	
198 5277	ePheSerLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlyS 215:	20 5
215 5227	<pre>ilProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeu 23 ::: ::: ::: CCCCAGCACAGAAGTTCATGTGAGAGCCATTAAAACTATGACT 51</pre>	1 78
232	leLysValPheLeuSe 24 ::::: TATATTTC 51	4 3
248 : 5142 :	SPheHisileArgArgPheIlePheLeu	02
261 5101 /	PhePheIleLeuVallleGlyIleTyrProSerGly 27 	52
273 I 5051 (HisSerLeuIleLeuIleLeuGlyAsnProLysLeuLysGlnAsnAlaLy 289 :: :: :: CACTCACTTATTTTAATTGTTTTAAATAATTAAATGCAGGCAG	5

```
JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                          primer_bind
BASE COUNT 2
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AF227135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_pr4:AF227135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                   alignment_block:
US-09-510-332-1 x AF227135
                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                            Align seg 1/1 to: AF227135
                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5001 CAGAATGCTG 4992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289 sLysPheLeu 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer_bind CDS
8 IleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAs
                                                                               AF227135 939 bp DNA PRI 18-MAR-2000
Homo sapiens candidate taste receptor T2R9 gene, complete cds.
AF227135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 939)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adler, E., Hoon, M.A., Mueller, K.L., Chandrashekar, J., Ryba, N.J.P. and Zuker, C.S. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF227135.1 GI:7262616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21-JAN-2000) NIDCR, prive, Bethesda, MD 20892, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A novel family of mammalian taste receptors Cell 100 (6), 693-702 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adler, E., Hoon, M.A., Mueller, K.L., Chandrashekar, J., Ryba, N.J. and Zuker, C.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 939)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"G protein-coupled receptor; PCR-derived sequence; similar to an interval in BAC AC006518"
/codon_start=1
/product="candidate taste receptor T2R9"
/protein_id-"aAR43908.1"
/protein_id-"AAR43908.1"
/translation="MPSAIEAIYIILIAGELTIGIWGNGFIVLVNCIDWLKRRDISLI
/translation="MPSAIEAIYIILIAGELTIGIWGNGFIVLVNUWTFANNSSLWFTSC
DIILISLAISRICLLCVISLDGFFWLKLFPGTYCNSVLVSIVNVWTFANNSSLWFTSC
LSIFYLLKIANISHPFFFWLKLKINKVWLAILLGSFLISLISVPKNDDMWYHLFKVS
HEENITWKFKVSKIPGTFKQLTLLLGVMVPFILCLISFFLLESLVRHTQORIRLHATG
FRDPSTEAHMRAIKAVIIFLLLLIVYYPVFLVMTSSALIPQGKLVLMIGDIVTVIFPS
FRDPSTEAHMRAIKAVIIFLLLLIVYTOFT DBUFFORT
                                                                                                                                                                                                                                                                                                                                                                                                 /product="candidate taste receptor T2R9" 919. .939 187 c 186 g 318 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHSFILIMGNSKLREAFLKMLRFVKCFLRRKKPFVP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="12"
/map="12p13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                            371.50
1.905
62.102
                                                                                                                                                                                                                                                                                                                                                                                                                                                               .>939
                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                            Length: 314
Gaps: 9
Percent Identity: 32.166
                                                                                                                                                                to: 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH, Bldg. 10 Room 1N106, 10 Center
```

315 T	267 1	250 u	37 . 121 C	20 r	03 g	87 L 71 T	70 sj 42 T	63 nA 92 CA	54 42 AA	37 al :: 19 TC	20 tA :: 72 AA)4 CY 22 TT	37 he 11 72 TT	'0 ePh 22 TAC	8 Le	1 et 2 TT
CATTI	1e	Lysp : CTGA	TCATC	gGlyA AGAGG	HisTh CACAC	euLeu ::::: TTATC	PThrLe AACCCT	laTh	AGAATG	SerMe	rgIle :: AGATC	sAla ACTO	IleAs GCCAA	hePheI ;;: CATATG	uGlnL GCTGT	AlaPr ::: TCCTT
1000 1::	yrPr	eHis : TCCT	Ty - - :GTGTA	laPro	rArgG : : : CAAGC	IlePh ::: CTTTG	euAla TGAAC	rIleG : TTGGA	GATGAT	tile : AATT	eSerLy ::: CAACAA	LysVa :: CAAGAT	nGlu ::: TAAT	leG :	euPh	oLeuA ::: GATTG
OSerG :		leAr	rPhe ::: CTAC	Ile :::	InMe :: AGAT	eLeu -	IleG1	ln :: AATTC	TATGT	CysVa	ysLeu ::: AGGTC	lalas : : AGCCA	LeuG1 :: TCAAG	Phe	Ile. ATAT	SpLe ::
CCA -	lyHis	gArgP :::: AAAAT	SerHi CCA	SerAla AGGGCC	tArgAs : TCGACT	heAl :::: TCTC	nIle ::: GGTG	AAAG	Ty GGTA	lPheHi	Ya::	erval	uLeuT : TCTCT	IleMe ::::: GTGCT	CATTA	uLeuL :::: CATCC
TCAT	SerL	heIl :::: TAGT	scys	LeuLeu ::: :ATAAAG	snThrV : TGCATG	avalL : : ATTTT	PheSe ::: ATG	TGAGT	rPheL	sse.	lProTrpMet : :CTTGCGAT	lArgH : ATCGC	rpLe :: GGTT	tCysS: - AGTAA	ହ :	LeuSer
CAI	euIle	ePheL ::::: GTTGA	MetIl ::::: GTCTT	uSer ::: GGCA	Vala :::: GCTA	euLe :: TCTT	rPhe	AAAAT	LeuArg	rLysT	MetIl ::::: ATTCT	isPro ACCCA	uAlaT ::::: TACTT	65 - 6	. Phe	CYSLe
CTAA	LeuI	LeuPhe :::::: ATGATT	eLysv : TCTTG	IleLe ::::: GTGAT	LaGly :: CAGGG	uLeuI : GTTAC	1A1		LysP AAAG	yral	eLeu : TCTG	LeuP ::: TTTT	hrTr :: CTTG	AlaAsnCys ATTGTGAAT	TYTVa ::::: TTTAT	euAla TGGCC
IMI	leLeu	PheI	/alPhe ::: GTTATG	uSer ; CATC	SerA TTCA	lePh :: TTTT	aGluP	AGGTAC	heP	aGlyP : A	GlySe GGGTC	helle ::: TCTTC	LeuG :	ysal :: ATGT	lasn : GCTG	Vals ::: ATCT
GGF	GlyAs	leLe ;; acat	eLeuS : GACCT	PheLe	rgVal GAGAC	eSerL	heSe	TTTC	hes : ATG	heMe :: TTAG	rLeu :::	TrpL	lyva: :::: GTAT	alleL :::: TGTCT	ValIl ::::: CTCTT	erArg CCAGA
-	nPr	uValIl:: : AGTAAC	SerSe 	uIle :::	ProG :	euGl TAGT	rVal .GTT	LysG.	erGln ::::: AAGAA	tvalp TGTTC	LeuTy	euLys TGAAG	1PheT:	euLe	eVal TCCA	Iler ATCI
\$	Lys	leG	rLe 	CTC	lyA :: GTA	a H	CCC	luA :: AGT	\$ - 8	S – g	/rV 1	Me 1	AT 3	AT — UP	<u>၂</u>	'ne 5
	283	267 814	250 764	236 720	220 670	203 620	186 570	170 541	163 491	153 441	137 118	20 371	03	87 271	70 221	7 71

```
Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein -
                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                   Post-processing:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein search, using sw model
 SPTREMBL_15:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel:
9: sp_plane:*
10: sp_plane:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebr
14: sp_unclass
                                                                                                                                                                                                                                                                 Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          March 15, 2001, 12:57:24; Search time 71 Seconds (without alignments) 493.594 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1521
1 MLESHLIIYFLLAVIQFLLG......GNPKLKQNAKKFLLHSKCCQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                      374700 seqs, 117207915 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-510-332-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                    sp_organelle:*
                                                                                                                                                  sp_invertebrate:*
                                                                                                                                                                                                     sp_bacteria:*
                                                                                                                                                                                                                    sp_archea:*
sp_vertebrate:*
sp_unclassified:*
                               sp_virus:*
                                                     sp_rodent:*
                                                                 sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                             374700
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SSER

Receptor. SEQUENCE

299 AA;

34333 MW; CFB17DD15645392C CRC64;

Query Match Best Local Similarity Matches 299; Conserv

100.0%; Score 1521; DB 4; Length 299; illarity 100.0%; Pred. No. 2.5e-97; Conservative 0; Mismatches 0; Indels 0

0;

Gaps

0

ţ	100	1 9	17	16	15	14	13	12	11	10	, 9	80	7	σ	G	4	ω	2	L	Result No.
0 . 0	310.5	יי	315.5	315.5	317	317.5	331.5	339.5	355.5	356	358	369	371.5	376	376	405	767	782	1521	Score
	20.4	20.6	20.7	20.7	20.8	20.9	21.8	22.3	23.4	23.4	23.5	24.3	24.4	24.7	24.7	26.6	50.4	51.4	100.0	Query Match Length
!	317	291	333	299	309	308	305	314	308	303	307	297	312	318	309	316	335	335	299	ength I
	4	4	11	4	1	11	11	11	11	4	4	11	4	4	4	4	=	11	4	DB
	8AAN60	09NYV7	Q9JKF0	Q9NYW4	QUARTS	Q9JKT9	Q9JKT7	Q9JKT6	Q9JKE7	6AAN60	OMAN 60	Q9JКЕ9	CANAM1	CHANGO	Q9NYW2	Q9NYW6	Q9JKU1	Q9JKT2	Q9NYW7	ID
	Q9nyv8 homo sapien	Q9nyv/ homo sapien	QSJRIO Factus noty	Solites and	עשייין אייים השיוסי	Calkta watthe both	(9) kt/ tattus 1101 v	Idetus	Q97ke/ raccus norv	Quyvy nomo sapren	Qynywo nomo sapren	Q9JKey ractus norv	Qynywr nollo sapren	Qynyws nomo sapien	Qunywz nomo sapren			DS: 1 This mascata		Description

멍 Q В QΥ 밁

Ş 밁

RT "A novel femily of mammalian taste receptors."; RT Cell 100:693-702(2000). DR EMBL; AF227129; AAF43902.1;	SEQUENCE FROM N.A. Adler E., Hoon M.A., Mueller K.L., Chandrashekar J.,	Homo Sapiens (Human). Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxID=9606;	AC Q9NYW/; DT 01-0CT-2000 (TrEMBLrel. 15, Created) DT 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) DT 01-0CT-2000 (TrEMBLrel. 15, Last annotation update) DT 01-0CT-2000 (TREMBLREL 15, Last annotation update) DE CANDIDATE TASTE RECEPTOR T2R1.	RESULT 1 Q9NYW7 ID Q9NYW7 PRELIMINARY; PRT; 299 AA.	ALIGNMENTS	5 120.5 7.9 342 12 090387	121.5 8.0 341 8 Q9MD83	122 8.0 352 13 Q91855	122.5 8.1 547 5 045965	124 8.2 500 8 Q9ZZQZ	124 8.2 346 13 QPUA9	125 8.2 352 13 QYIBS6	6 8.2 287 13 Q9PT44	130.5 8.6 310 11 Q9WUU2	134 8.8 410 13 Q9PW33	217.5 14.3 238 11 Q9JKA3	230.5 15.2 243 11 Q9JKA2	237.5 15.6 245 11 09JKA4	242.5 15.9 246 11 Q9JKAO	264.5 17.4 297 11 Q9JKT3	289 19.0 309 11 09.JKT0	294 19.3 300 11 Q9JKT4	
	Ryba N.J.P.,	<pre>Euteleostom1; Homo.</pre>				kaposi	Q9md83 drosophila O70269 rattus norv		045965 caenorhabdi	Q62853 rattus norv		Q9xuk8 caenorhabdi		Q9ptx9 brachydanio		Q9jke8 rattus norv		Sum	09jka0 mus musculu	mus	rattus	Q9jkt4 mus muscutu	

4

```
Š
                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                      ACC OCC OT DIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
Q9JKT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ş
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 154; Conserv
                                                                                 OJJKU1 PRELIMINAKI;
OJJKU1,
OJJKU1,
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R1.
Adler E., Hoon M.A., Mueller C.S., zuker C.S., novel family of mammalian Cell 100:693-702(2000).
                                  SEQUENCE FROM N.A. Adler E., Hoon M.A.,
                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9JKT2 PRELIMINARY; PRT; 335 AA.
09JKT2;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R19.
                                                                NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adler E., Ho
Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "A novel family of mammalian taste Cell 100:693-702(2000).
                                                                                                                                                                                                   238
                                                                                                                                                                                                                                       181
                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF227149; AAF43922.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-129/SVJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                          1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQL
                                                                                                                                                                       ω
                                                                                                                                                                                             N
                                                                                                                                                                                                                                  --GLTLPFLIFTVAVLLLLSSLMNHSRQMR-TMVGTREPSRHALVSAMLSILSFLILYLS
                                                                                                                                                                                                                                             VAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALLSILSFLILYFS
                                                                                                                                                                                                                                                                       RISRLVPWLILASVVYVTVTTFIHSRETSELPKQIFISFFSKNTTRVRPAHATLLSVFVF
                                                                                                                                                                                                                                                                               RISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLRKFESQNAT-IQKEDTLAIQIFSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MMEGHMLFFLLVVVVQFLTGVLANGLIVVVNAIDLIMWKKMAPLDLLLFCLATSRIILQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoon M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     335 AA;
                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    37734 MW;
                                                                                                                                                                                                                                                                                                                                                                                              51.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mueller K.L.,
                                                                                                                                                                                                                                                                                                                                                                                     51;
                                  K.L.,
                                                                                                                                                                                                                                                                                                                                                                                              Score 782; DB 11; Length Pred. No. 1.2e-46;
                  taste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                   1399C323FC7CE645 CRC64;
                receptors.";
                                  Chandrashekar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chandrashekar J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                     90;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                      Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi; 
; Murinae; Mus
                                  Ryba N.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ryba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N.J.
                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                       Rattus
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                296
                                                                                                                                                                                                                 298
                                                                                                                                                                                                                                                     239
                                                                                                                                                                                                                                   237
                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                                                                                                                                                                                                   <u>ω</u>
                                                                                                                                                                                                              멍
                            Q
                                                  멂
                                                                   Qy
                                                                                    Вb
                                                                                                       8
                                                                                                                            В
                                                                                                                                           Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q
                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                Query Match
Best Local Similarity
Matches 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 155; Conser
                                                                                                                                                                                                                                                                                                                                                                         Q9NYW6;
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
               184
                                169
                                                   124
                                                                                                                                                                                                                                                                                                                                                                                                                                238
                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                            œ
                                                                                                                                               œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
            LGTL------WYLPPLIVSLASYSLLIFSLGRHTRQMLQNGTSSRDPTTEAHKRAIR
                             EDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALL
                                                WRVSRVMVWMLLGALLLSCGSTASLINEFKLYSVFRGIEATRNVTEHFRKKRSEYYLIHV
                                                                 MRISKLVPWMILGSLLY------VSMICVFHSKYAGFMVPYFLRKFFSQNATIQK
                                                                                                                                                                                                               316 AA;
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
```

```
SQ
                                                                                                                                                                                                                                             Addler E., Hoon M.A., Mueller K
Zuker C.S.;
Zuker C.S.;
"A novel family of mammalian to
Cell 100:693-702(2000).
EMBL; AF227130; AAF43903.1; -.
                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
CANDIDATE TASTE RECEPTOR T2R3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF227140; AAF43913.1; Receptor. SEQUENCE 335 AA; 37851 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---FLIEFSPNTHDSGIIMQIIDVSWTFTNHLSIWLATCLGVLYCLKIASFSHPTFLWLK
                                                                 VFLILSGTQFTLGILVNCFIELVNGSSWFKTKRMSLSDFITTLALLRIILLCIILTDS-
                                                                                             IYFLLAVIQELLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNV
                               IVIFFIEFIMCSANCAILL-----FINELELWLATWLGVFYCAKVASVRHPLFIWLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYMVAVLISTQVLYLGSRTFVFCLLVIGMYPSIHSIVLILGNPKLKRNAKMFIVHCKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HCMIKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RISRLVPWLILGSVLYVIITTFIHSRETSAILKPIFI-SLFPKNAT-QVGTGHATLLSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CILFAQLCLESLVRHTLEEDNITEVFIINELSLWEATWLGVFYCAKIATIPHPLELWLKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIFYVNVIVIFFIEFINCSANCAILLEINELELWLATWLGVFYCAKVASVRHPLFIWLKM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RISKLYPHMILGSLLYVSMICVFHSK-YAGEMYPYFLRKFFSQNATIQKEDTLAIQIFSF
                                                                                                                                                                                                                                                                                                                    Hoon M.A., Mueller K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                     35914 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37851 MW;
                                                                                                                              26.6%; Score 405; DB 4; 36.4%; Pred. No. 8.1e-21; tive 43; Mismatches 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 767; DB 11;
Pred. No. 1.3e-45;
i3; Mismatches 87;
                                                                                                                                                                                                                                                                                    taste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                     6A7BA3C6497ABC5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AB8A1CEDDE70C12C
                                                                                                                                                                                                                                                                                                                  Chandrashekar J.,
                                                                                                                                                                                                                                                                                receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                  114; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
                                                                                                                                                                Length
                                                                                                                                                                                                                   CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                  Ryba
                                                                                                                                  42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٨
                                                                                                                                                                                                                                                                                                                    .
P.
                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298
                               119
                                                                                                67
123
                                                                 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
```

234

183 168

Q

SILSE---LILYFSHCMIKVFLSSL-KFHIRRFIFLFFILVIGIYPSGHSLILIIGNPKL

284

```
RESULT
Q9NYW2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      몽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ъ
                                                                                                                                                                   ٧٥.
                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                             RESULT
Q9NYW3
                                                                                                                                                                                                    Вb
                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                            뮹
 В
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9NYW2 PRELIMINARY; PRT; 309 AM.
O9NYW2;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
CANDIDATE TASTE RECEPTOR T2R8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "A novel family of mammalian taste Cell 100:693-702(2000). EMBL; AF227134; AAF43907.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adler E., F
Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                235 IILSFFFLFLLYFLAFLIASFGNFLPKTKMAKMIGEVMTM---FYPAGHSFILILGNSKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                     OPNYM3;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R7.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel-Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo NCBI_TaxID=9606;
                                                                                                    Q9NYW3
                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                        162
                                                                                                                                                                                                                                                                                               127
                                                                                                                                                                                                                                                                                                                   123
                                                                                                                                                          281
                                                                                                                                                                                273
                                                                                                                                                                                                      229
                                                                                                                                                                                                                           222
                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                           œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KQT---FVVMLRC 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KONAKKFLLHSKC
                                                                                                                                                                                                                                                                                                                                                                                    DMVVHWILLGCFAISLLVSLIAAIVLSCDYRFHAIAKHKRNITEMFHVSKIPYF-----
                                                                                                                                                                                                                                                                                                                  SKLVPWMILGSL---LYVSMICV-----FHS-----KYAGFMVPYFLRKFFS 161
                                                                                                                                                                                                                                                                                                                                                             IVIFFIEFIMCSANCAILL-----FINELELWLATWLGVFYCAKVASVRHPLFIWLKMRI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                 101;
                                                                                                                                                                                                    VHVRAIKTMTSFIFFFFLY----YISSI---LMTFSYLMTKYKLAVEFGEIAAILYPLG
                                                                                                                                                                                                                                                                                                                                         APISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL------FFILVIGIYPSG
                                                                                                                                                                                                                                                                     QNATIQKEDTLAIQIFSEVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRG
                                                                                                                                                                      HSLILILGNPKLKQNAKKFL 292
                                                                                                                                                         HSLILIVLNNKLRQTFVRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hoon M.A., Mueller K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                 EPLTLFNLFAI-----VPFIVSLISFFLLVRSLWRHTKQIKLYATGSRDPSTE 228
                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35877
                                                                                                                                                                                                                                                                                                                                                                                                                                              24.7%;
                         Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                     56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 376; DB.4
Pred. No. 7.7e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5E3D94B726A52413
                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chandrashekar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309
                                                                                                       318
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB .4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                      101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ryba N.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .
'v
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                                                                                            66
                                                                                                                                                                                                                                                                             221
                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                             280
                                                                                                                                                                                                                                 272
                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
```

```
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         멂
                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
Q9NYW1
                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                               Ş
                                                                      밁
                                                                                            Q
δõ
                        멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                     Query Match
Best Local S
Matches 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A., Mueller K.L., Ch
Adler E., Hoon M.A., Mueller K.L., Ch
Zuker C.S.;
"A novel family of mammalian taste re
cell 100:693-702(2000).
EMBL; AF227133; AAF43906.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                       QNYW1;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
CANDIDATE TASTE RECEPTOR T2R9.
                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     Q9NYW1
                                                                                                                                                                                                     "A novel family of mammalian taste receptors."; Cell 100:693-702(2000).
EMBL; AF227135; AAF43908.1;
                                                                                                                                                                                                                                          Adler E., E
Zuker C.S.;
                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 WILLGCV----VLSVFISLPATENLNADFRFCVKAKRKTNLTWSCRVNKTQHASTKLFLN
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 YYLSFLIATSSYFMPETELAVIFGESIALIYPSSHSFILILGNNKLRHASLKVI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 YPDVYATGKEMRIIDFFWTLTNHLSIWFATCLSIYYFFKIGNFFHPLFLWMKWRIDRVIS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIVIF
  124
                                                                                                                                Local Similarity
                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                            7
                                                                                                œ
                                                                        æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WMILGSLLYVSMICVFHSKYA------GFMVPYFLRKFFSQNATIQKEDTLAIQIFSF 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIEFIMCSANCAILLFI----NELELWLATWLGVFYCAKVASVRHPLFIWLKMRISKLVP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LATL-LPFCVCLMSFFLLILSLRRHIRRMQLSATGCRDPSTEAHVRALKAVISFLLLFIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HCMIKVFLSSLKFHIRRFIFLFFILVIG-IYPSGHSLILILGNPKLKQNAKKFL
                                                                       IYFLLAVIQELLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFI----F 63
                                                YVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKMRIS 123
KLVPWMILGSLLYVSMICVFHSKYAGFMVP-----YFLRKF-FSQNATIQ------
                         FMLLFPGTYGNSVLVSIVNVVWTFANNSSLWFTSCLSIFYLLKIANISHPFFFWLKLKIN
                                                                                                                        100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 32.7
96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoon M.A., Mueller K.L., Chandrashekar J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 AA;
                                                                                                                                                                                                                                                        Hoon M.A.,
                                                                                                                                                                                 312 AA;
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36549 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.7%; Score 376; DB 4; 32.7%; Pred. No. 7.9e-19;
                                                                                                                                                                                   35611 MW;
                                                                                                                                  24.4%;
                                                                                                                                                                                                                                                          Mueller K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60;
                                                                                                                         60;
                                                                                                                                     Score 371.5; DB Pred. No. 1.6e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F187ADB2D8274B8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 120;
                                                                                                                                                                                    CCE66F1E31051F49
                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptors.";
                                                                                                                                                                                                                                                          Chandrashekar
                                                                                                                                                                                                                                                                                                                                                                                                          312
                                                                                                                                                                                                                                                                                                                                                                                                         ĄΑ
                                                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                 DB 4;
                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 318;
                                                                                                                                                                                       CRC64
                                                                                                                                                                                                                                                          J., Ryba N.J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                Length
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ryba
                                                                                                                                                     312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                             39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292
                                                                                                                                                                                                                                                              .
.
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187
                                  127
           167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
```

```
RESULT
Q9NYWO
ID QS
AC QS
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULPT
OPJACE
ON
AC
ON
DT
ON

                                                                                                                                                                                    B
                                                                                                                                                                                                                         S
                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                   용
                                                                                                                                                                                                                                                                                                                                                                                                           ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                             рь
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 104; Conserv
O9NYWO PRELIMINARY;
Q9NYWO;
01-OCT-2000 (Tremburel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9JKE9 PRELIMINARY; PRT; 297 AA. Q9JKE9; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update) 01-OCT-2000 (TrEMBLrel. 15, Last annotation update) TASTE RECEPTOR RT2R6 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                               285
                                                                                                                                                                                                                            292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF240766; AAF45304.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A novel family of mammalian taste receptors."; Cell 100:693-702(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adler E., H
Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                      173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123
                                                                                                                                                                                                                                                                            225
                                                                                                                                                                                                                                                                                                                      233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 LLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIVIFFIEFIM |:|| | | :|: : :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       w
                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LTER
                                                                                                                                                                                                                                                                                             FLILYFSHCMIKVFLSSLKFHIR-RFIFLFFILVIGIYPSGHSLILILGNPKLKQNAKKF 291
                                                                                                                                                                                                                                                                                                                                                         LCRVK
                                                                                                                                                                                                                            LLHSK 296
                                                                                                                                                                                                                                                                  FLVLFIVYCLAFLIATSSYFMPESELAVIWGELIALIYPSSHSFILILGNSKLKQASVRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                   L--ILSLC-----FSLPVTENLADDFRRCVKTKERINSTLRCKLNKAGYASVKVNLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSANCAILLFI----NELELWLATWLGVFYCAKVASVRHPLFIWLKNRISKLVPWMILGS 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RGKEMRIIDEFWTLTNHLSVWFATCLSIFYFFKIANFFHPLFLWIKWRIDKLILRTLLAC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVGILGNAFIALVNEMGMMKNRKITAIDLILSSLAMSRICLQCIILLDCIILVQYPDTYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLSILSFLILYFSHC-MIKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILILGNPKLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QNAKKFLLHSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IKAVIIFLLLIVYYPVFLVMTSSALIPQGKLVLMIGDIVTVIFPSSHSFILIMGNSKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FKQLTLNLGVM-----VPFILCLISFFLLLFSLVRHTKQIRLHATGFRDPSTEAHMRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -KEDTLATQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRGAPISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KVMLAILLGSFL-ISLI-----ISVPKNDDMWYHLFKVSHEENITWKFKVSKIPGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAFLKMLRFVKC
                                                                                                                                                                               289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hoon M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 1
297 AA; 34107 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24.3%; Score 369; DB 11;
ilarity 34.1%; Pred. No. 2.2e-18;
Conservative 51; Mismatches 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mueller K.L.,
          15,
          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          873D0440C2863E25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chandrashekar
                                                         307
                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ت.
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ryba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         232
                                                                                                                                                                                                                                                                                                                                                                                                                                                        172
                                                                                                                                                                                                                                                                                                                                                         224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
```

```
Q
                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
   Query Match
Best Local S
Matches 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 31.0
                                                                                                                                                                                                               O9NYV9
O9NYV9;
O9NYV9;
O1-OCT-2000 (TrEMBLrel. 15, Created)
O1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
O1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R13.
                                                                                   "A novel family of mammalian Cell 100:693-702(2000). EMBL: AF227137; AAF43910.1;
                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                SEQUENCE
                                                                                                                        Adler E., H
Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    u1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R10.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
McBi_TaxID=9606;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A novel family of mammalian taste Cell 100:693-702(2000). EMBL; AF227136; AAF43909.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            290
                                                                                                                                                                                                                                                                                                                                                                                                    230
                                                                                                                                                                                                                                                                                                                                                                                                                                   170 EYFIKQILLNLGVIFFFTLSLITCIFLIISLWRHNROMQSNVTGLRDSNTEAHVKAMKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 IYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                            RVLQQLKCCE 299
                                                                                                                                                                                                                                                                                                                                                                  KFLLHSKCCQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                    --FVAEFSVPL-LIFLFAV-----LLLIFSLGRHTRQMRNTVAGSRVPGRGAPISALLSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTNMVLPFMIV--FLLISSLLNF-----AYIAKILNDYKT--KNDTVWDLNMYKS
                                                                                                                                                                                                                                                                                                                                                                                      ISFIILFILYFIGMAIEISCFTVRENKLLLMFGMTTTAIYPWGHSFILILGNSKLKQASL 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLRKFFSQNATIQKEDTL-AIQIFS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIQIFSPNIYASGN--LIEYISYFWVIGNQSSMWFATSLSIFYFLKIANFSNYIFLWLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFIFVVVSESVFGVLGNGFIGLVNCIDCAKN-KLSTIGFILTGLAISRIFL-IWIIITDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IVIFFIEFIMCSANCAILLFI-----NELELWLATWLGVFYCAKVASVRHPLFIWLKM
                                                                                                                                    Hoon M.A.,
                                                              303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hoon M.A., Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307
                                                              Α
,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA:
                                                              35118 MW;
23.4%; Score 356; DB 4; 31.9%; Pred. No. 1.8e-17; tive 69; Mismatches 116
                                                                                                                                 Mueller K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35365 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68; Mismatches 110;
                                                                                                             taste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 358; DB 4;
Pred. No. 1.3e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.L.,
                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                            756BF5382E36BFB5 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              058DD69A55AE71C6 CRC64;
                                                                                                          receptors.";
                                                                                                                                    Chandrashekar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chandrashekar J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptors.";
                        Length 303;
                                                                                                                                J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 307;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                  Ryba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ryba N.J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36;
                                                                                                                                                                                                                                                                                                                                                                                                             289
                                                                                                                                                                                                                                                                                                                                                                                                                                                             230
                                                                                                                                                                                                                                                                                                                                                                                                                                      229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
```

97; Conservative

116;

Indels

22;

Gaps

11;

286 QNAKKFLL 293

```
RESULT
Q9JKE7
ID Q9
DT Q9
DT 01
DT 01
DT 01
DT 01
DT 01
RP RA
OS RA
OS RA
OX NC
CM MA
RA AC
RA A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                  84.
                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                            QY
                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
밁
                                        δÃ
                                                                                                밁
                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O9JKE7;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
TASTE RECEPTOR RT2R12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adler E., Hoon M.A., Mueller K.L., zuker C.S.;
"A novel family of mammalian taste Cell 100:693-702(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9JKE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF240768; AAF45306.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 AFLL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                   170
                                                                                                                                                                                                      120
                                                                                                                                                                                                                                                      116
                                                226
233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                          سر
                                                                                                                                                                                                                                                                                                                                                                                                          _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EILVSWFLALHYLAIFVSGTGLRIMIFSWIVSNHFNLWLATIFSIFYLLKIASESSPAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIFYVNVIVIFFIEFIMCSANCAILLF----INELELWLATWLGVFYCAKVASVRHPLFI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MESALPSIFTLVIIAEFIIGNLSNGFIVLINCIDWVSKRELSSVDKLLIILAISRIGLIW 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLILY--FSHCMIKVFLSSLKFHIRRFIFLFFILVIGIY-PSGHSLILILGNPKLKQNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSVKFTMTMFSLTPFTVAFISFLLLIFSLQKHLQKMQLNYKGHRDPRTKVHTNALKIVIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YLKWRVNKVILMILLGTLVFLFLNLIQINMHIK--DWLDRY--ERNTTWNFSMSDFETFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WLKMRISKLVPWMILGSL--LYVSMICV-FHSKYAGFMVPYFLRKFFSQNATIQKEDTLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LESHLIIYFLLAVI-QFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLLFYASFFLCVLISWISEL---YQNTVIYMLCETIGVFSPSSHSFLLILGNAKLRQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQL 60
                          ALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILILIGNPKLK 285
                                                                                                                                                                                                   LWLKWRFPALVPWLLLGSIL-VSFIVTLMFFWGNHTVYQA-----FLRRKFSGNTTF-KE
                                                                                                                                                                                                                                                                                                    CVGLVNSFYYSLHLVEYSRSLARQLISLHMDFLNSATFWFGTWLSVLFCIKIANFSHPAF 119
                                                                                                                                                                                                                                                                                                                                                                                                       DTLAIQIFSF----VAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRGAPIS
                                                                                                                                                                                                                                              IMLKMRISKLVPWMILGSLLYVSMICVF-----HSKYAGFMVPYFLRKFFSQNATIQKE 169
                                                                                                                                                                                                                                                                                                                                                  FIFYVNVIV--IFFIEFIMCSANCAILL---FINELELWLATWLGVFYCAKVASVRHPLF 115
ALKSLISFLVLYALSYVSMVIDATVVISSDNVWYWPWQIILYLCMSVHPFILITNNLKFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36009 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.4%; Score 355.5; DB 11; Length 31.8%; Pred. No. 1.9e-17; tive 56; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CF78D1487D75990C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chandrashekar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ryba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.J.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289
                                                                                                           232
                                                                                                                                                           225
                                                                                                                                                                                                              172
          292
```

```
OPERATOR OF THE STATE OF THE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δδ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                      RESULT
Q9JKT7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
  AC OC OC RN RA RA RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adler E., Ho
Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09JKT6;
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-OCT-2000 (TrEMBLrel. 15, Last annotation
                                                                                                                                                              Q9JKT7;
Q1-QCT-2000 (TrEMBLrel. 15, Created)
Q1-QCT-2000 (TrEMBLrel. 15, Last sequence up
Q1-QCT-2000 (TrEMBLrel. 15, Last annotation
CANDIDATE TASTE RECEPTOR T2R7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "A novel family of mammalian Cell 100:693-702(2000). EMBL: AF227145; AAF43918.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rāt).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CANDIDATE TASTE RECEPTOR T2R8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9ЈКТ6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
                                                                                                                                                                                                                                                                                                                  Q9ЈКТ7
Adler E., Hoon M.A.,
Zuker C.S.;
                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 WLKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLRKFFSQNATIQKEDTLAIQI 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                                                                                                                                                                                                       285 LKQTSLWILSHLKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       284 LKQNAKKFLLHSKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 LLAVIQELLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTFRQLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YLKWRLKQVIVGMLLASLVFL------PGILMQRTLEERPYQYGGNTSEDSMETDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSSSFIFGMKLQILYF-AWILSS-----HFSLWFATALSIFYLLRIANCSWKIFL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --QLFIFYVNVIVIFFIEFIMCSANCAILLFINELELMLATWLGVFYCAKVASVRHPLFI 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMVSFLLLYTSY-----FLSLLISWIAQKHHSKLVDIIGIITELMYPSVHSFILILGNSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AKFTELILFNMTIFSVIPFSLALISFLLLIFSLWKHLQKMQLSSRGHGDPSTKAHRNALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FSF-----VAEFSV-PLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALL 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SILSFLILYFSHCMIKVFLSSL----KFHIRRFIFLFFILVIGIYPSGHSLILILGNPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hoon M.A., Mueller K.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22.3%;
31.2%;
                                                                                                                       Chórdata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                            298
                            Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 339.5; DB Pred. No. 2.5e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   taste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                            X.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299D9B3DAACCE6FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chandrashekar J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptors.";
                              Chandrashekar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    314
                                                                                                                                                                                                                                                                                                                            305
                                                                                                                                                                                                                                                                                                                         ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
                                                                                                                                                                                                                        on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                 J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ryba N.J.P
                                 Ryba N.J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                    Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
```

```
Ş
                                              В
                                                                    Š
                                                                                               망
                                                                                                                 Ş
                                                                                                                                            B
                                                                                                                                                                      á
                                                                                                                                                                                                                                                                  ACC OCC DITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RT DR RT
                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 89; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        O9JKT9 PRELIMINARY; PRT; 308 AA.
O9JKT9;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R4.
                                                                                                                                                                                                                                                                                    "A novel family of mammalian taste receptors Cell 100:693-702(2000) EMBL: AF227142: AAF43915.1; -.
                                                                                                                                                                                                                                                                                                                                                                                       Rettus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                            Adler E., H
Zuker C.S.;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "A novel family of mammalian taste receptors."; Cell 100:693-702(2000). EMBL; AF227144; AAF43917.1; -. Receptor. 305 AA; 35594 MW; 533BABD8C8BA4BE9
Ļ
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-10116;
                      179
                                        128 --VVFIFLSGCLLTSWLLCFPQFSKMLNNSKMYWGNTSWLQQQKNVFLINQSLTNLGIFF
                                                                       124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 MIMESVTPETVALVSFILLIESLWKHLQKMHLSSRGERDPSTKAHVNALRIMVSELLLYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 VAEFSV-PLLIFLEAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALLSILSFLILYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 RISKLVPWMILGSLLYVSM-ICVFHSKYAGFMVPYFLRKFFSQNATIQKEDTLAIQIFSF 179
                                                                                                                        69
                                                                                                                                                                       11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 AWLKYMKYSFSYLAGTELRVMMLTWVVSNHFSLWLATILSIFYLLKIASFSRPVFLYLKW
                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
  FVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALLSILSFLILYF
                                                                KLVPWMILGSLLYVSMICVF--HSKYAGFMVPYFLRKFFSQ---NATIQKEDTLAIQIFS 178
                                                                                        QVFF-PHILTEGNITEYITYIWVFLNHLSVWFATNLNILYFLKIANFSNSVFLWLKSRVR
                                                                                                         VIFFIEFIMCSANCA-----ILLFINELELMLATWLGVFYCAKVASVRHPLFIWLKMRIS 123
                                                                                                                                     LLAVI--QFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVI 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVKKVLLLILLGNLIFLMFNILQINTHIEDWMDQY--KRNITWDSRVNEFVGFSNLVLLE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IYFLLAVI---QFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFL--QLFI 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FYVNVIVIFFIEFIMCSANCAILLFI--NELELWLATWLGVFYCAKVASVRHPLFIWLKM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 28.7
86; Conservative
                                                                                                                                                                                                                                                                                                                                     Hoon M.A., Mueller K.L., Chandrashekar
                                                                                                                                                                                                                                                              308 AA; 35052 MW;
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35594 MW;
                                                                                                                                                                                                             20.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.8%; Score 331.5; DB 11; 28.7%; Pred. No. 8.5e-16;
                                                                                                                                                                                                61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78;
                                                                                                                                                                                            Score 317.5; DB 11; Lengtl
Pred. No. 7.8e-15;
1; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                             00BC4193204EF043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            533BABD8C8BA4BE9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                                                                                                                                                                                                                                                                                                                     J.,
                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                     Ryba
                                                                                                                                                                                                                                                                                                                                     N.J.P.,
                                                                                                                                                                                              25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                                                                                       Rattus
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                 238
                                         185
                                                                                                                                            89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
```

```
RESULT 15
Q9JKT5
ID 9JKT5
AC Q9JKT5
DT 01-OCT
DT 01-OCT
DT 01-OCT
DT 01-OCT
DC CANDID
OS RATLUS
OC EUKARY
OC EUKARY
OC MAMMAI
OX NCBI_T
RN [1]
RN [1]
RP SEQUEN
RA ZUKER
RA ZUKER
RA ZUKER
RA ZUKER
RA ZUKER
RA COLL:
DR EMBL;
SQ SEQUEN
                              Š
                                                              В
                                                                                        δ
                                                                                                                          밁
                                                                                                                                                       ρ
                                                                                                                                                                                          망
                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                      Вb
                                                                                                                                                                                                                                                                                                                                             δĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 91; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9JKT5 PRELIMINARY; PKT; 3U7 AA.
Q9JKT5;
Q1-CCT-2000 (TrEMBLrel. 15, Created)
Q1-CCT-2000 (TrEMBLrel. 15, Last sequence update)
Q1-CCT-2000 (TrEMBLrel. 15, Last annotation update)
CANDIDATE TASTE RECEPTOR T2R9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adler E., Hoon M.A., Mueller K.L., Chandrashekar Zuker C.S.;
"A novel family of mammalian taste receptors.";
Cell 100:693-702(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF227146; AAF43919.1;
   282
                                                                                                                               174
                                                                                                                                                                                                                          112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                               221
                                                                                                                                                            161
                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298 CCE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186
                                                                                                                                                                                                                                                                                                                                   1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQL
                                                                                                                                                                                                                                                                                                                        L
                              GNPKLKQNAKKFL 292
                                                                                     GAPISALLSILSFLILYFSHCM-IKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILIL
                                                                                                                        TSNYVL----INIGVISL-----LIMTLTACFLLIISLWKHSRQMQSNVSGFRDLNT
                                                                                                                                                                                     HYIFLWLKRRIDKVFAFLLWCLLISWAI--SFSFTVKVMKSNPKNHGNRTSGTHWEKREF
                                                                                                                                                                                                                                                                     FIFYVNVIVIFF------IEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                   MLSAAEGILLSIATVEAGLGVLGNTFIALVNCMDWAKNKKLSKIGFLLFGLATSRIFIVW
TNSQLKQAFVKVL
                                                          EAHVKAIKFLISFIILFILYFIGVAVEIICMFIPENKLLFIFGLTTASVYPCCHSVILIL
                                                                                                                                         HPLFIWLKMRISK------LVPWMILGSLLYVSMICVFHSKYAGFMV--PYFLRKFF 160
                                                                                                                                                                                                                                                     ILILDAYAKLFFPGKYLSKSLTEIISC-----IWMTVNHMTVWFATSLSIFYFLKIANFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SHCMIKVELSSLKFHI--RREIFLFEILVIGIYPSGHSLILILGNPKLKQNAKKFLLHSK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FI----IVSLITCFLLIVFLWRHIRQMHSDGSGLRDLNTEAHVKAMRVLISFAVLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LH-FVGLSIQVLCFFLPQNNLLFITGLIATCLYPCGHSIILILGNKQLKQASLKALQHLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 AA;
                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                35149 MW;
                                                                                                                                                                                                                                                                                                                                                                                              20.8%;
                                                                                                                                                                                                                                                                                                                                                                             %; Score 317; DB 11; Length 3
%; Pred. No. 8.5e-15;
61; Mismatches 121; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0FCE43EB9D3F0090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chandrashekar J.,
                                                                                                                                                                                                                                                                                                                                                                                                               Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ryba N.J.P.,
                                                                                                                                                                                                                                                                                                                                                                                 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus
                                                            281
                                                                                        279
                                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238
                                                                                                                                                                                                                                                                                                                                                                                 8;
```

Search completed: March 15, 2001, 13:19:12 Job time: 1308 sec

THIS PAGE BLANK AUST

```
Title:
Perfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on:
   Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        score:
131
130.5
129.5
128.5
128.5
128.5
128.5
128.5
128.5
128.5
128.5
128.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
129.5
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  March 15, 2001, 12:58:00 ; Search time 71.14 Seconds (without alignments) 135.731 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88757 segs, 32294092 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-510-332-1
1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SwissProt_39:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GenCore version Copyright (c) 1993 - 2000
    MLESHLIIYFLLAVIQFLLG......GNPKLKQNAKKFLLHSKCCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
   DB
 OPSD_PHOVI
OPSD_PIG
NUZM_DROMA
OPSD_MACFA
OPSD_MOUSE
OPSD_GLOME
OPSD_GLOME
OPSD_GLOME
OPSD_GLOME
OPSD_GLOME
OPSD_CANFA
OPSD_CANFA
OPSD_CANFA
OPSD_SCYCA
OPSC_CARAU
OPSD_LAMJA
                                                                                                                                                                                                                                                                                                OPSD_HUMAN
OPSD_DELDE
GP41_HUMAN
                                                                                                                                                                                                                                                                                                                                           OPSD_MESBI
OPSD_TURTR
O2C1_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                     OPSD_CRIGR
OPSD_RAT
OPSD_BUFBU
                                                                                                                                                                                                                                                                                                                                                                                                                                           NU2M_APILI
OPSD_RABIT
OPSD_SHEEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                  OPSD_RAJER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88757
                                                                                                                                                                                                                                                                                                                                                                                                    p49912 oryctolagus
p02700 ovis aries
p79863 raja erinac
p28681 cricetulus
p51489 rattus norv
    062792
P51471
051750
098146
015529
P32308
P32314
Q90214
Q90214
P22671
P11168
P412679
P12336
                                                                                                                                                                                                                                                       P56514
062793
062798
095371
P08100
062791
014843
062794
P29867
                                                                                                                                                                                                            Q28886
P15409
O62796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P34849 apis mellif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                     1 homo sapien
0 homo sapien
1 delphinus d
3 homo sapien
4 phoca vitul
6 sus scrofa
                                                                                                                                                                                                                                                                                                                                                            bufo bufo (
mesoplodon
tursiops tr
      trichechus
globicephal
anolis caro
borrelia bu
kaposi's sa
homo sapien
canis famil
anguilla an
gsyliorhinu
carassius a
lampetra ja
homo sapien
yanopus laee
phoca groen
rattus norv
                                                                                                                                                                                                                                           drosophila
macaca fasc
                                                                                                                                                                                                                               mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299
```

DE RESERVA		
_APILI _APILI NUZM_APILI NUZM_APILI NUZM_APILI P34849; P9249 Q33787; Q33788 Q1-FEB-1994 (Q1-FEB-194 (Q1-FEB-19	Ü	88888444444444444444444444444444444444
APILI NUZM_APILI NUZM_APILI NUZM_APILI P34849; p9 301-FEB-199 APIS melli Mitochondr Eukaryota; Pterygota; Ptery		1:6 116 116 116 116 115 115 115 115 114 114
APILI ANA APILI AP	÷	1444.55.155.17
APILI APILI APILI Q33787; Q33788; Q33787; Q33788; Q33787; Q33787; Q33788; Q33787; Q33788; Q01-FEB-1994 (Rel APIS mellifera 1 Mitochondrion. Elwaryota; Metazy Pterygota; Neopt Rolline-96114603 CROZIER R.H., Grozier R.		111111111111
APILI APILI NUZM_APILI NUZM_APILI NUZM_APILI NUZM_APILI P34849; p92496; p92497; p33787; Q33788; Q35885; Q33788; Q35885; Q337878; Q35885; Q1.FEB-1994 (Rel. 28, La. 30.MAP.2000 (Rel. 39, La. 30.MAP.2000 (Rel. 29, La. 30.MAP.2000 (Rel. 29, La. 30.MAP.2000 (Rel. 20, La. 20.MAP.2000 (Rel. 20, La. 20, La. 20.MAP.2000 (Rel. 20, La. 20, La. 20.MAP.2000 (Rel. 20, La. 20, La. 20, La. 20.MAP.2000 (Rel. 20, La. 20,	;	J. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.
STANDARD; ; P92497; ; Q36885; ; Q37886; ; Q37886; ; Q37886; ; Q37886; ; Q4886; ;	7	354 354 354 353 353 353 353 353
The properties of the contract		4440000000
		SD S
P92886; P929 ence update) tation update tation update CHAIN 2 (EC 1 n honeybee). Tracheata; Hymenopt pe honeybee Ap ne honeyb	ALIGNMENT	GALML DROME BOVIN BOVIN BOVIN ANOCA CHICK COTIN RAT COTIN
33 AA 2886; P92: ion update) ion updatt IN 2 (EC oneybee). acheata; Hymenop ; Hymenop bee subsp aguence."; 1996). 1996). 1996). SenBank/Di IOUINONE L MEMBRANI L MEMBRANI L MEMBRANI L Sichion forma tute. Th as Long th Treeved ment (Seee ib.ch).	ENTS	Z PPXPZCZPWC
nce update) stion update) stion update) stion update) stion update) honeybee). Tracheata; Hexapoda; ta; Hymenoptera; Apo phoneybee Apis melli ,"; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;		
Apis mell Apis mell Apis datal PROTECT NAD(+) NE PROTECT PRODUCT SUBUNIT 2 Froduced at its d. Usage e http://		
; Q33785; (; Q33785; (; appoda; Insapoda; In		
3). 3). 3). 3). 3). 3). 3). 3). 3). 3).		09 09 09 09 09 09 09
Insecta; rita; Acules rita; Acules is mellifera is mellifera is mellifera is mellifera is mellifera is mellifera dubiquinol. MITOCHONDRI AMILY		093441 P03896 042604 P25104 Q9yh04 P02699 P41591 P28683 Q98980 042330
3786; Sta; Aculeat complete complete cHONDRIAN cHONDRIAN charaction for collimation for co- sib.ch/		
Aculeata; Aculeata; INOL. HONDRIAL HONDRIAL HONDRIAL Outstab MBL outstab MBL outstab Accitions o A collabo MBL outstab MBL out		
. = = = 0 = 0 +		us mela ophila faber faber taurus odus vu taurus caro us gall omyzon pus lae us norv
n its oo way necroin tounce/		

```
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
VARIANT
VARIANT
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
₽70
                                                                                                                                                                    169
                                                                                                                                                                                                                   163
                                                                                                                                                                                                                                                                    125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPRO01750; -. PFAM; PF00361; oxidored_q1;
                                                                                                                                                                                                                                                                                                                104
                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                              54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G
                                                                                                                                                                                                NATIQKEDTLAIQIFSFVAE-----FSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRV
                                                                                                                                                                                                                                                                                 CAKVASVRHPLFIWLKM-RISKLVPWMILGSLLYVSMICVFHSKYAGFWVPYFLRKFFSQ 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L) U35762 AAB30241.1 CJ U35764 AAB30244.1 CJ U35764 AAB30244.1 CJ U35765 AAB30244.1 CJ U35765 AAB30244.1 CJ U35765 AAB30244.1 CJ U35765 AAB30177.1 CJ U75280 AAB41179.1 CJ U75281 AAB41180.1 CJ U75282 AAB41181.1 CJ U75285 AAB41181.1 CJ U75286 AAB41183.1 CJ U75286 AAB41183.1 CJ U75286 AAB41184.1 CJ U75286 AAB41184.1 CJ U75286 AAB41185.1 CJ U75289 AAB41185.1 CJ U75289
                                                                                                     PGRGAPISALLSILSFLILYFSHCMIKVFLS-----SLKFHIRRFIFLFFILVIGIY
                                                                                                                                                    KKLLACSTIFNSFYFIFILELNKNMFIAMIILYSFNYFLLISFLNKFNIQNFNFMFYNK-
                                                                                                                                                                                                                                                          MSTLIKF-IPIYMMVSMTKINSWTLYFLITNSLYIS-----
                                                                                                                                                                                                                                                                                                                                                SSIFL-FFMIIVYLSSISFTKTDTFNEMVQMMFFLKIGTFPFHFWMIYSYEMMNWKQIFL 124
                                                                                                                                                                                                                                                                                                                                                                                               SRIFLQLFIFYVNVIVIFFIEFIMCSANCAILLFIN----ELELW------LATWLGVFY 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HWEIYFLITIFVLMMNSNNIFIQWMLMEF--GTIISISLIN-IKSTNKTPSLIYYSVSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLIIYFLLAV-----IQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAV 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U35749
U35751
U35752
U35752
U35753
U35755
U35756
U35757
U35757
U35757
U35757
U35760
U35761
U35762
U35762
U35763
U35763
U35763
U35763
U35763
U35763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 19.9
67; Conservative
                                                      ----YOMYTELTLMENYSNYPIELSEVIKWNLIEMMVSVKAYNWILELLMISSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142
158
203
262
333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB38231.1
AAB38232.1
AAB38233.1
AAB38234.1
AAB38235.1
AAB38235.1
AAB38236.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB38238.1;
AAB38239.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142
158
203
262
40879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.6%;
19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ubiquinone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSP. CARNICA, SSP. IDERICA, SSP.

INTERMISSA, SSP. LAMARCKII, SSP. SSP.
MACEDONICA, SSP. MEDA, SSP. MONTICOLA,
SSP. SAHARIENSIS, SSP. SCUTELLATA AND
SSP. SICULA).

V -> M (IN HAPLOTYPE 9).

T -> I (IN HAPLOTYPE 3, 5, 6, 7 AND 10)
V -> I (IN HAPLOTYPE 4, MELLII AND
W -> I (IN HAPLOTYPE 4, MELLII AND
MELLI2).

K -> S (IN SSP. LAMARCKII).
I -> T (IN MELLII).

F -> L (IN SSP. CARNICA).

V -> D (IN HAPCOTYPE 6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 131; DB 1 Pred. No. 0.018;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> L (IN SSP. CARNICA).
-> D (IN HAPOLTYPE 6).
866969F11529907F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion; Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (IN SSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADANSONII, SSP.
                                                                                                                                                                                                                                                     ----FYANKFYTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 AND 10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAPENSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                         277
                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
```

ORRADO DE PROPERTA DE LA CARRA DE PROPERTA DE LA CARRA DEL CARRA DE LA CARRA DEL CARRA DE LA CARRA DEL CARRA DEL

.6

```
PRESULT

OPSD_RABIT

ID OPSD_RA

AC P49912

DT 01-OCT

OC OFFICE

RHODOW

RC STRAIN

RA MCDUNN

RA MCDUNN

RA MCDUNN

RA MCDUNN

RA MCDUNN

RA MCDUNN

RO STRAIN

RA MCDOW

The d

RT Photor

RL Gene 1

CC -!- TI

CC -!- TI

CC -!- ME

CC -!- ME

CC -!- MI

CC -!- SI

CC OT Seen

CC -!- SI

CC OT Seen

CC --- MI

CC ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPRO00276; -.
INTERPRO; IPRO00732; -.
INTERPRO; IPRO00732; -.
INTERPRO; IPRO0071760; -.
PEAM; PFO0001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00239; OPSIN.
PRINTS; PR002579; RHODOPSIN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS00238; OPSIN; 1.
                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPSD_RABIT
P49912;
01-OCT-1996
01-OCT-1996
15-JUL-1999
                                                                           TRANSMEM
                                                                                                                    TRANSMEM
                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                            Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                    Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCRDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U21688; AAA91640.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    photoreceptors.";
Gene 162:331-332(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   McDowell J.H.;
"The deduced amino-acid sequence of opsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith W.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-NEW ZEALAND WHITE; TISSUE-RETINA; MEDLINE-96032368; PubMed-7557454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryctolagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 LMIWNYIIILKRVFLKMNFYKNNFIDDKDNKYMYHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINKED TO CIS-RETINAL.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
VISION IN DIM LIGHT.
PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE PHOSPHORYLATED.
MISCELLANEOUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMA AT 495 I
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCR_1573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us cuniculus (Rabbit).
; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
       37
62
74
99
114
113
153
177
203
231
253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martinko J.M., Wheeler J.N., Hargrave P.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 34, Created)
(Rel. 34, Last sequence update)
(Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                    Retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                            Lipoprotein;
    36
61
73
98
113
1133
152
176
202
230
252
276
                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                            1 (POTENTIAL).
CYTOPLASMIC.
2 (POTENTIAL)
2 (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC.
4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                          Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348
                                                                                                                                                                                                                                                                                                                                                                                              --
                                                                                                                                                                                                                                                                                                                     G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ⋧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from rabbit rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              313
                                                                                                                                                                                                                                                                                                                  Glycoprotein; Vision;
tein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥
```

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
멍
                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                RESULT 3
OPSD_SHEEP
                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
DOMAIN
MOD_RES
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIPID
                                                                                                                                                                                                                                                           P02700;
21-JUL-1986
01-FEB-1991
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING
    [3]
SEQUENCE OF 240-348.
MEDLINE-82013638; PubMed-7278988;
Findlay J.B.C., Brett M., Pappin |
Findlay J.B.C. Brett M. | Pappin |
                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
Bovidae; Caprinae; Ovis.
                                                               SEQUENCE OF 1-111 AND 144-239.

MEDLINE=83282605; PubMed=6224479;
Brett M., Findlay J.B.C.;

"Isolation and characterization of the CNBr proteolytically derived N-terminal fragment Biochem. J. 211:661-670(1983).
                                                                                                                                                                                                                             Ovis aries
                                                                                                                                                                                                                                                   RHODOPSIN
                                                                                                                                                   Pappin D.J.C.,
"A structural m
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112
                                                                                                                                                                                                                                                                                                                                                            307
                                                                                                                                                                                                                                                                                                                                                                                 278
                                                                                                                                                                                                                                                                                                                                                                                                                           222
                                                                                                                                                                                                                                                                                                                                                                                                                                                200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162
 "Primary structure rhodopsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLAAYM---FLLIVLGFPINFLTLYVTV-----OHKKLRTPLNYILLNLAVADLFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----HPL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFS
                                                                                                                                                                                                                                                                                                                                                           IMMNKQF----RNCMLTTICC
                                                                                                                                                                                                                                                                                                                                                                                                     VTRMVIIMVIAELICHVPYASVAFYIETHQGSNEGPIEMTIPAFFAKSSSIY---NPVIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QNATIQKEDTLAIQIFSEVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGENHAIMGVAFTWI-MALACAAP-PLVGWSRYIPEGMQCSCGIDY-----YTLKPEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LGGFTTTLYTSLHGYFVFGPTGCNVEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
                                                                                                                                                                                                                                                                                                        _SHEEP
                                                                                                                                                                                                                                                                                                                                                                                ILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                        APISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLIL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       l Similarity
70; Conserv
                                                                                                                                        D.J.C., Elipoulos E., Brett M., Findlay ctural model for ovine rhodopsin."; Biol. Macromol. 6:73-76(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            285
310
1
1
5
15
296
296
322
323
110
343
                                                                                                                                                                                                                              (Sheep).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                           (Rel. 01, Created)
(Rel. 17, Last sequence up
(Rel. 38, Last annotation
                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                -IYMEVVHFTIPLIIIFFCYGQLVFTVKEAAAQQQES-ATTQKAEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             343
38994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
2
15
296
296
322
323
187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (POTENTIAL).
CYTOPLASMIC.
ACETYLATION (BY SIMILARITY).
N-LINKED (GLCNAC. .) (BY SIN
N-LINKED (GLCNAC. .) (BY SIN
RETINAL CHROMOPHORE.
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                             323
                                                                                                                                                                                                                                                                                                                                                                                  298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 130.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
             D.J.C.;
functional
                                                                                                                                                                                                                                                              update)
on update)
                                                                                                                                                                                                                                                                                                          348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .02;
                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128;
                                                                             peptides of ovine
               sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.
                                                                                                                                                                 4
                                                                                                                                                                   .
E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
               in
                                                                                                                                                                   Ġ
                                                                              opsin.";
                                                                                          from
                 ovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                             Bovoidea;
                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
```

```
SALE ELECTE ELEC
                                                                      Вþ
                                                                                                 QY
                                                                                                                                        밁
                                                                                                                                                                           δÃ
                            δÃ
밁
                                                                                                                                                                                                               Query Match
Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence variability in the retinal-attachment do
rhodopsins."
Biochem 1. 217:605-613(1984)
FINCTION: VISUAL PICHENTS ARE THE LIGHT-ABSORB
FINCTION: VISUAL PICHENTS OF AN APOPROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 293:314-316(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO;
INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A:
GCRDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pappin D.J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RETINAL BINDING S. MEDLINE-84178280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO0237; GPCRRHODOPSN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                      MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPR001760; -.
PFAM; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>'</del>-
                                                                                                                                                                                                                                                                                                                                                              TIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Photoreceptor; Retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
148
                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINKED TO CIS-RETINAL.
SUBGELLUAR LOCATION: INTEGRAL
TISSUE SPECIFICITY: ROD SHAPED
VISION IN DIM LIGHT.
                                                                                                        9
                                                                                                                                          39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPSIN SUBFAMILY.; A30407; OOSH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTM: SOME OR ALL OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THIS SIMILARITY: BELONGS
                                                                                                                                                                               \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE PHOSPHORYLATED
                                                                                                                                                                         MLESHLIIYELLAVIQELLGIETNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ
                                                                                                      LFIFYVNVIVIFFIEFINCSANCAILLFI ---- NELELW ---- LATWLGVFYCAKVASVR 111
                                                                                                                                            MLAAYM---FLLIVLGFPINFLTLYVTV--
                                                                    FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
FGENHAIMGVAFTWVMALACAAPPLVGW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCR_0194;
                                                                                                                                                                                                                 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; IPR000276; -.; IPR000732; -.; IPR000732; -.
                                  -HPL----FIW----LKMRISKLVPWMILGSLLYVSMICVFHSKYAGEMVPYFLR---
                                                                                                                                                                                                                                                                                                        343
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1
62
74
99
114
134
153
177
203
231
253
277
285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Findlay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SITE.
                                                                                                                                                                                                                                                                                                          A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=6370231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THIS
                                                                                                                                                                                                                                                                                                            343
38891
                                                                                                                                                                                                                                      8.5%;
21.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oī
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .B.C.; the retinal-attachment domain of
                                                                                                                                                                                                                                                                                                              WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOXYL-TERMINAL SER
                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC...) (BY SIN
N-LINKED (GLCNAC...) (BY SIN
RETINAL CHROMOPHORE,
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORVLATION (BY RK) (BY SIMILARITY).
                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL)
                                                                                                                                                                                                                   Score 129.5; DB 
Pred. No. 0.023; 
52; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC.
6 (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Glycoprotein; Vision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAS AN ABSORPTION MAXIMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEMBRANE PROTEIN.
PHOTORECEPTOR CELLS WHICH MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGHT-ABSORBING MOLECULES THAT N APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                ----QHKKLRTPLNYILLNLAVADLFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein
                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                        125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OR.
                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THR
                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESIDUES
         -IPQGMQCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammalian
                                                                                                                                                                                                                                                             348;
                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΑT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor
                                                                                                                                                                                                                          71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               495
                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥
                                                                               147
                                                                                                                                                        87
                                                                                                                                                                                        59
                                               157
```

16;

```
PRESULT PRESULT OF ACCORDED TO THE PRESULT OF AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                           PRINTS: PR00237; GPCRHODDPSN.
PRINTS: PR00238; OPSIN.
PRINTS: PR00579; RHODOPSIN.
PROSITE: PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE: PS50262; G_PROTEIN_RECEP_F1_2;
PROSITE: PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                       INTERPRO;
INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                    entitles
or send a
                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and this statement is not removed. Usage by and the statement is not removed.
                                                                                                                                                                                                                                                          INTERPRO; IPR001760; -. PFAM; PF00001; 7tm_1; 1
                                                                                                           Phosphorylation;
                                                                                                                                                                                                                                                                                                                                         EMBL; U81514; AAC60251.1; GCRDB; GCR_1485; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <del>: :</del>
                                                                                                                                   Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAJER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Raja erinacea (Little skate).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Squalea; Hypnosqualea; Pristiorajea; Batoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-RETINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rajiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P79863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPSD_RAJER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE PHOSPHORYLATED.
MISCELLANEOUS: THIS RHODOPSIN HAS A
SIMILARITY: BELONGS TO FAMILY 1 OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPSIN SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPTFMTIPAFFAKSSSVY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVPGRGAPISALLSILSFLILVFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALYFTLKPEINNE----SFVIYMFVVHFSIPLIVIFFCYGQLVFTVKEAAAQQQES-ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NPVIYIMMNKQF----RNCMLTTLCC
                                                                                                                                                                                                                                                                                                                                                                                                      an
                                                                                                                                                                                                                                                                                   requires a license agreement (So
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rajidae;
                1
37
62
74
99
                                                                                                                           Retinal protein; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                           Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35,
              36
61
73
98
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                .•
          1 (POTENTIAL).
CYTOPLASMIC.
2 (POTENTIAL).
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opsin cDNA from the skate retina.";
                                                                                    : Palmitate; G-protein EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354
                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AN ABSORPTION MAXIMA
F G-PROTEIN COUPLED RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                               --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SER OR THR RESIDUES
                                                                                                                       Glycoprotein; Vision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELLS
                                                                                                       coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPSIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     he EMBL outstation restrictions on it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COVALENTLY
                                                                                                     receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                     s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AT 501
                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                n no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215
```

```
RESULT
OPSD_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OS
THE TENT OF THE PART OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 70
                                                                                                                                                                                                                                                                                                                                                                       OPSD_CRIGR
P28681;
01-DEC-1992
01-DEC-1992
15-JUL-1999
      <del>+</del> <del>+</del> <del>+</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRIGR
                                                   Gale J.M., Tobey R.A., D'Anna A.;
"Localization and DNA sequence of a replication in rhodopsin gene locus of Chinese hamster cells.";
J. Mol. Biol. 224:343-358(1992).
-i- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSO MEDIATE VISION. THEY CONSIST OF AN APOPROTEI
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                               Cricetulus griseus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                          RHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                             MEDLINE~92219256; PubMed-1560457;
                                                                                                                                                                                                    TISSUE=OVARY;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                            Cricetulus.
                                                                                                                                                                                                                                                                                                                                                           RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44
  LINKED TO CIS-RETINAL.
SUBCELLULAR LOCATION: INTEGRAL
TISSUE SPECIFICITY: ROD SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 IYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQLFIFYVN 66 ::||: | | : | | | | :|: | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVYNPLIYILMNKQFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---HSLILILGNPKLK 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL-----FFILVIGIYPSG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----FIWLKMRIS----KLVPWMILGSLLYVSMICVFHSKYAGFWVPYFLR-----KFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIVIFFIEFIMCSANCAILLFI----NELELWLATWLGV----FYCAKVASVR----HPL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MFFLI-----LTGLPVNFLTLFVT----IQHKKLRQPLNYILLNLAVSDLFMVFGGFTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VTRMVIIMVVAELICWVPY-----ASVAF----YIFINQGCDFTPFFMTVPAFFAKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKPEVNNE---SFVIYMFVVHFTIPLIVIFFCYGRLVCTVKEAAAQQQESESTQRAE-RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IITSMNGYFIFGPAGCNFEGFFATLGGEVGLWCLVVLAIERYMVVCKPMANFRFGSQHAI 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                         2 (Rel. 24,
2 (Rel. 24,
9 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114
153
153
153
177
203
231
253
277
285
310
310
310
310
327
310
310
310
327
327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                  (Chinese hamster).
; Chordata; Craniata; Vertebrata; Euteleostomi;
; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133
152
176
202
230
230
276
284
284
309
354
157
187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.5%;
                                                                                                                                                                                                                                                                                                                                                                           Last
Last
                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WW.
                                                                                                                                                                                                                                                                                                                                                                         annotation
                                                                                                                                                                                                                                                                                                                                                                                            sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 (POTENTIAL).
CYTOPLASMIC.
N-LINKED (GLCNAC. . .) (POTE
N-LINKED (GLCNAC. . .) (POTE
RETINAL CHROMOPHORE (BY SIMI
PALMITATE (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (POTENTIAL)
CYTOPLASMIC.
4 (POTENTIAL)
EXTRACELLULAR
5 (POTENTIAL)
CYTOPLASMIC.
6 (POTENTIAL)
EXTRACELLULAR
7 (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 129.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1ACEB918ADA214C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
PHOTORECEPTOR
                    MEMBRANE PROTEIN
                                                     HE LIGHT-ABSORBING AN APOPROTEIN, OPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      348
                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SRY----IPEGLQCSCGVDYYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        107;
                                                                                                                                  origin
CELLS WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .) (POTENTIAL).
.) (POTENTIAL).
(BY SIMILARITY).
                                                     OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                    'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83;
MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
```

```
Ş
                                            밁
                                                               QΥ
                                                                                        밁
                                                                                                             δÃ
밁
                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0237; GPCRHODDSN.
PRINTS; PRO0238; OPSIN.
PRINTS; PR00579; RHODDPSIN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
DISULFID
BINDING
                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPR001760; -. PFAM; PF00001; 7tm 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X61084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO;
                                                                                                                                                                                               MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO;
                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                    TIPID
                                                                                                                                                                                                                                                                                         MOD_RES
                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
 148
                       112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMA AT 495 I SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VISION IN DIM LIG
PTM: SOME OR ALL
                                                                   60
                                                                                         39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE PHOSPHORYLATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S23398;
                                                                                                              MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                         MLAAYM---FLLIVLGFPINFLTLYVTV-----QHKKLRTPLNYILLNLAVADLFMV
FGENHAIMGVVFTWI-MALACAAP-PLVGWSRYIPEGMQCSCGVDY-----YTLKPEVN
                      ----HPL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFS 161
                                                                  LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                             FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVICKPMSNFR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCR_0412;
                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR000276; -. IPR000732; -.
                                                                                                                                                                                                348 AA;
                                                                                                                                                                                                                                                                                                    1
62
74
99
114
134
153
177
203
231
253
277
285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S23398.
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAA43398.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Retinal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LIGHT.
ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES
                                                                                                                                                                                                                       15
187
296
322
323
                                                                                                                                                                                                 39097
                                                                                                                                                   8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .'
                                                                                                                                                                                                 MW;
                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                               3 (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                   Score 128.5; DE Pred. No. 0.027;
                                                                                                                                                                                                PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PHOSPHORYLATION (BY RK) (BY SIMILARITY).
ASCDF27804F30AA1 CRC64;
                                                                                                                                                                                                                                                        ACETYLATION (BY SIMILARITY)

N-LINKED (GLCNAC...) (BY S

N-LINKED (GLCNAC...) (BY S

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                    7 (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR.
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Palmitate;
                                                                                                                                                                                                                                             RETINAL CHROMOPHORE
                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transmembrane; Glycoprotein; Vision;
                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G-protein
                                                                                                                                                                DB 1;
                                                                                                                                           129;
                                                                                                                                                                 Length
                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coupled receptor;
                                                                                                                                                                                                                                                                       SIMILARITY).
SIMILARITY).
                                                                                                                                                                  348;
                                                                                                                                            59;
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ¥
                                                                                                87
                                                                                                                                              16;
```

```
RESULT OF DEAD BRADER B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996
01-OCT-1996
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPSD_RAT P51489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _RAT
                                                                                                                                                                INTERPRO; IPRO00276;
INTERPRO; IPRO00732;
INTERPRO; IPRO01760;
IPROM; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY; TISSUE-RETINAL MEDLINE-95383121; PubMed-7654522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 QNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200
                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams T.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huber A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Mol. Neurosci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barnstable C.J., Morabito M.A.; "Isolation and coding sequence of the J. Mol. Neurosci. 5:207-209(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250
                      PROSITE;
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produ
between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                           PRINTS; PR00237; GPCRRHODOPSN. PRINTS; PR00238; OPSIN. PRINTS; PR00579; RHODOPSIN.
                                                                                                                                                                                                                                                            GCRDB; GCR_1446;
GCRDB; GCR_1458;
                                                                                                                                                                                                                                                                                                                  EMBL; U22180; AAA84439.1; EMBL; Z46957; CAA87081.1;
  Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NESFV-----IYMFVVHFTIPLIVIFFCYGQLVFTVKEAAAQQQES-ATTQKAEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LINKED TO CIS-RETINAL.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES
VISION IN DIM LIGHT.
PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISCELLANEOUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMA AT 495 NM. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTRMVILMVVFFLICWFPYAGVAFYIFTHQGSNFGPIFMTLPAFFAKSSSIY---NPVIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMNKQF----RNCMLTTLCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE PHOSPHORYLATED
                      PS00237; G_PROTEIN_RECEP_F1_1; 1. PS50262; G_PROTEIN_RECEP_F1_2; 1. PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baker B.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 (Rel. 34, 15 (Rel. 34, 17) (Rel. 38, 17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                           7 tm_1;
     Retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sander P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-RETINA;
     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
          Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerdon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G., Paulsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   opsin
          Glycoprotein; Vision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                           .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              way
```

TRANSMEM DOMAIN TRANSMEM DOMAIN

TRANSMEM DOMAIN

TRANSMEM DOMAIN

Phosphorylation; Acetylati

õ

ж Р

```
Bufo bufo (European toad).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                               302 -NPITYIMMNKQF----RNCMLTSLCC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLESHLIIYFLLAVIQFLLGIFTNGTIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ
                                                                                                                                                                                                                                                                       GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                              QKAEKEVTRMVIIMVIFFLICWLPYASVAMYIFTHQGSNFGPIFMTLPAFFAKTASIY--
                                                                                                                                                                                                                                                                                                                        RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS
                                                                                                                                                                                                                                                                                                                                                  GIDYYTLKPEVNNE---SFVIYMFVVHFTIPMIVIFFCYGQLVFTVKEAAAQQQES-ATT
                                                                                                                                                                                                                                                                                                                                                                             --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS
                                                                                                                                                                                                                                                                                                                                                                                                        FGENHAIMGVAFTWVMALACAAPPLVGW------SRY----IPEGMQCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                 ----HPL----FIW---LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIGLWSLVVLAIERYVVVCKPMSNFR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLAAYM---FLLIVLGEPINFLTLYVTV-----QHKKLRTPLNYILLNLAVADLEMV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity 20.5
67; Conservative
                                                                                                                                                                                STANDARD;
                                                                                                                      36, Created)
36, Last sequence update)
39, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipoprotein; Palmitate; G-protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 s
                                                     Anura; Neobatrachia; Bufonoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC.

ACETYLATION (BY SIMILARITY),
N-LINKED (GLCNAC. ...) (BY SIMILARITY).
N-LINKED (GLCNAC. ...) (BY SIMILARITY).
RETINAL CHROMOPHORE.
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64; Mismatches
                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 128.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC.

2 (POTENTIAL).

EXTRACELLULAR.

3 (POTENTIAL).
                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR
5 (POTENTTATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (BY RK) (BY S -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC.
4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 (POTENTIAL).
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DA0F3F90C30984BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                          298
                                                                                                                                                                             354
                                                                                                                        update)
                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 348;
                                                   Bufonidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                              215
                                                                                                                                                                                                                                                                                                30
                                                                                                                                                                                                                                                                                                                           271
                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                        187
                                                                                                                                                                                                                                                                                                                                                                                                                                   157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
        밁
                               Ş
                                                            멍
                                                                                    Ş
                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 74; Conserv
                                                                                                                                                                                 DISULFID SEQUENCE
                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                         LIPID
                                                                                                                                                                                                                                         BINDING
                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00238; OPSIN; 1.
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatic
the European Bioinformatics Institute. These
use by non-profit institutions as long a
modified and this statement is not removed.
entities requires a license agreement (See
                                                                                                                                                                                                              CIPID
                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR001760; -. PFAM; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPRO00276; INTERPRO; IPRO00732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCRDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U59921; AAB93704.1;
                                65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>-</del>
        93
                                                            37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               functional comparisons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Rhodopsins from three frog and toad species: sequences and functional commarisons ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fyhrquist N., Donner K., Hargrave P.A., McDowell J.H., Popp Smith W.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98288405; PubMed-9533857;
                                                                                       9
VTMYSSMNGYFILGATGCYVEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFRFSENH
                         VNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR----H 112
                                                   YSILCAYMFLLILLGFPINEMTLYVT----IQHKKLRTPLNYILLNLAFANHFMVLCGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . Eye Res. 66:295-305(1998).
FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY LINKED TO CIS-RETINAL. THIS RECEPTOR IS COUPLED TO THE ACTIVATION OF PHOSPHOLIPASE C.
                                                                             YFLLAVIQF---LLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQLFIFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES
BE PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCR_2484;
                                                                                                                                                                                354 AA;
                                                                                                               Conservative
                                                                                                                                                                                                              203
231
253
277
285
285
310
310
320
323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lipoprotein;
                                                                                                                                                                                 187
39777
                                                                                                                           8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                Ψ×.
                                                                                                              57;
                                                                                                                                                                                                                               7 (POTENTIAL).
CYTOPLASMIC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
RETINAL CHROMOPHORE.
                                                                                                          Score 128.5; DB 1;
Pred. No. 0.027;
7; Mismatches 130;
                                                                                                                                                                                                                                                                                                                 2 (POTENTIAL).

EXTRACELLULAR.
3 (POTENTIAL).
CYTOPLASMIC.
4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL).
CYTOPLASMIC
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC.
2 (POTENTIAL
                                                                                                                                                                          PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
BY SIMILARITY.
; 35C99992101AC919 CRC64;
                                                                                                                                                                                                                                                                                           6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR.

1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein; Vision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                            نن
                                                                                                                                   Length
                                                                                                           Indels
                                                                                                                                                                                                                                             (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρĄ
                                                                                                                                                                                                                                             SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                     354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTORS
```

Matches Query Match Best Local

MOD_RES CONFLICT SEQUENCE

Ą

DISULFID

CARBOHYD CARBOHYD BINDING

MOD_RES DOMAIN TRANSMEM DOMAIN TRANSMEM TRANSMEM

ω

collaboration -

MAY

for ctions on

15

5

its

LIPID

LIPID

RHODOPSIN

55;

Gaps

16;

92 64

Eukaryota; Amphibia; B

Batrachia;

Bufo.

SEQUENCE FROM N.A

15-JUL-1998 15-JUL-1998 30-MAY-2000

(Rel. (Rel. (Rel.

OPSD_BUFBU P56514; BUFBU δõ 밁 Š 밁 S В Ş 밁 Ş 밁 Š

272 244 188

148 112

```
. Proceeds and process of the contraction of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPSD_MESBI
062793;
15-DEC-1998
15-DEC-1998
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MESBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fasick J.I., Robinson P.R.;
submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Fasick J.I., Robin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113
                                  TRANSMEM
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mesoplodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mesoplodon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153
                                                                                                                                                                                                                                                                                                                                           INTERPRO; IPRO00276; INTERPRO; IPRO00732; INTERPRO; IPRO01760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309
                                                                                                                                                                                    PROSITE; PS00237;
PROSITE; PS50262;
PROSITE; PS00238;
                                                                                                                                                                                                                                                                                                                      PFAM; PF00001; 7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send
                                                                                                                                                                                                                                                          PRINTS;
                                                                                                                                                                                                                                                                                                 PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF055316; AAC12763.1; -.
                                                                                                   DOMAIN
                                                                                                                                             Phosphorylation;
                                                                                                                        Acetylation.
                                                                                                                                                                  Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINKED TO CIS-RETINAL.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WH.
TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WH.
VISION IN DIM LIGHT.
PPM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR
BE PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IIMVVFFLICWVPYASVAFFIFSNQGSEFGPIFMTVPAFFAKSSSIY---NPVIYIM---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLSILSFLILTESHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLILILGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----IYMFVVHFTIPLIIIFFCYGRLVCTVKEAAAQQQES-ATTQKAEKEVTRMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRGAPISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AVMGVAFTWI-MALSCAVP-PLLGWSRYIPEGMQCSCGVDY-----YTLKPEVNNESFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFSQNATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -LNKQFRNCMITTLCC
                                                                                                                                                                                                                                                   PR00237; GPCRRHODOP
PR00238; OPSIN.
PR00579; RHODOPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
(Rel.
(Rel.
                    1
37
62
74
99
                                                                                                                                                                  37; G_PROTEIN_RECEP_F1_1;
62; G_PROTEIN_RECEP_F1_2;
38; OPSIN; 1.
Retinal protein; Transmen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37,
37,
38,
                                                                                                                                                                                                                                                                                                 GPCRRHODOPSN.
                                                                                                                                                  Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Eutele Cetartiodactyla; Cetacea; Odontoceti;
                    36
61
73
98
113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence up
                EXTRACELLULAR.

1 (POTENTIAL).

CYTOPLASMIC.

2 (POTENTIAL).

EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                               Palmitate; G-protein
                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Usage
                                                                                                                                                      Glycoprotein;
tein coupled r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WHICH MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESIDUES MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ziphiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
                                                                                                                                                         receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                way
```

```
SOO SET THE FIRST THE FIRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Бр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                             OPSD_TURTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
  CCCCCRTAN RP RAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIPID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
DISULFID
BINDING
LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                             OPSD_TURTR
062798;
15-DEC-1998
15-DEC-1998
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOD_RES
FASICK J.I., ROBSINSON P.R.;

PASICK J.I., ROBSINSON P.R.;

MACCHARISM of spectral tuning in the dolphin visual pi
Biochemistry 37:433-438(1998).

1- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING
1- FUNCTION: THEY CONSIST OF AN APOPROTEIN, OPS
LINKED TO CIS-RETINAL.

LINKED TO CIS-RETINAL.

-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=98129138; PubMed=9471225;
                                                                                                                                                                                                                  Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                            RHO
                                                                                                                                                                                                                                                                                            RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
                                                                                                                                                                                               Tursiops.
                                                                                                                                                                                                                                                     Tursiops truncatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            306 YIMMNKQF----RNCMLTTLCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 YFLLAVIOFL---LGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLOLFIFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FSVLAAYMFLLIMLGFPINFLTLYVT----VQHKKLRTPLNYILLNLAVANLFMVLGGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PL----FIW---LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR-----KFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTLYTSNHAYFIFGPTGCNLEGFFATLGGEIALMSLVVLAIERYVVVCKPMSNFRFGENH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR----H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIMGLALTWIMALACAAPPLVGW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVTRMVVIMVVAFLICWVPYASVAFYIFTHQGSNEGPIFMTIPSFFAKSSAIY---NPVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
67; Conservat
                                                                                                                                                                                                                  ; Metazoa;
Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                 (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                 37,
37,
38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
15
187
187
296
296
322
323
                                                                                                                                                                                                                  (Atlantic bottle-nosed dolphin).
; Chordata; Craniata; Vertebrata; Eutel.
; Cetartiodactyla; Cetacea; Odontoceti;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.3%;
                                                                                                                                                                                                                                                                                                                 Last sequence up
                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (POTENTIAL).
CYTOPLASMIC.
4 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACEDUC.
7 (POTENTIAL).
CYTOPLASMIC.
CYTOPLASMIC.
ACETYLATION (BY SIMILARITY).
TNKED (GLCNAC. ..) (BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 125.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PHOSPHORYLATION (BY RK) (BY F83010DC40C450D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
BY SIMILARITY.
RETINAL CHROMOPHORE.
                                                                                               in the dolphin visual pigments.";
                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                     on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----SRY----IPEGMQCSCGVDYY
                                                                                                                                                                                                                                                                                                                                                                                                  348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.042
                                                                                                                                                                                                                                                                                                                                                                                                  Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                               Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
                                                                                                                                                                                                                          Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
```

OPSIN,

MOLECULES

COVALENTLY

```
В
                                                                             B
                                                                                                    ş
                                                                                                                              В
                                                                                                                                                 Ş
                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL: AF055456; AAC12940.1; -.
INTERPRO; IPR000276; -.
INTERPRO; IPR000732; -.
INTERPRO; IPR0007760; -.
PFAM; PF00001; 7tm.1; 1.
PFINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                                                                                                                                                 CARBOHYD
CARBOHYD
DISULFID
                                                                                                                                                                                                                                       MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                    DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                        BINDING
                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                CIPID
                                                                                                                                                                                                                                                                              LIPID
                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -
                                                                              97
                                                                                                      69
                                                                                                                              5
                                                                                                                                                     10
TLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALLSI
                                                                        TSLHAYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFRFGENHAIMG
                                                                                             VIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR----HPL--
                                                                                                                       FLLIVLGFPINFLTLYVTV------QHKKLRTPLNYILLNLAVANLFMVFGGFTTTLY
                                                                                                                                     FLLAVIQFLLGIFINGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQLFIFVVNVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES VISION IN DIM LIGHT.

PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES MAY
                         LALTWIMAMACAAAP--LVGWSRYIPEGMQC-----SCGIDYYTSR------QEVN
                                               --FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFSQNATIQKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE PHOSPHORYLATED (B
SIMILARITY: BELONGS
                                                                                                                                                                            64;
                                                                                                                                                                           Similarity 20.0
64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                               1
62
74
99
114
1134
153
177
203
277
285
210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Retinal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lipoprotein;
                                                                                                                                                                                                                                                                         1
2
15
187
296
322
                                                                                                                                                                                                                                                                                                                                                                                  36
61
73
98
113
113
152
176
202
230
230
                                                                                                                                                                                    8.2%;
                                                                                                                                                                                                                                       39093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YB)
                                                                                                                                                                                                                   CYTOPLASMIC.

CYTOPLASMIC.

ACETYLATION (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (BY SIMILARITY).

N-LINKED (GLCNAC. . .) (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

RETINAL CHROMOPHORE.

RETINAL CHROMOPHORE.

PALMITATE (BY SIMILARITY).

PALMITATE (BY SIMILARITY).

PHOSPHORYLATION (BY RK) (BY SIMILARITY).

PHOSPHORYLATION (BY RK) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY).
TO FAMILY 1 OF G-PROTEIN
                                                                                                                                                                                                                                      MW;
                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                                                                                                                                                                              3 (POTENTIAL).
CYTOPLASMIC.
4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL)
                                                                                                                                                                                     Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR.
5 (POTENTTAT)
                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR.
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n; Transmembrane; Glycoprotein; Vision; Palmitate; G-protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                           Mismatches
                                                                                                                                                                                     125;
No. 0.
                                                                                                                                                                                     DB 1;
                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUPLED
                                                                                                                                                                        Indels
                                                                                                                                                                        56;
                                                                                                                                                                      Gaps
  230
                                                170
                                                                         156
                                                                                                                       96
                         199
                                                                                                                                                89
                                                                                                                                                                        14;
```

S

õ

```
RESULT 10
OCAL_HUMAN
OID COST_HAM
AC 095371
DT 01-027
DT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                            1.0021.HUMAN STANUARL,
095371;
01-0CT-2000 (Rel. 40, Created
01-0CT-2000 (Rel. 40, Last sc
01-0CT-2000 (Rel. 40, Last a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fischel-Ghodsian N., Kastner D.L.;
Construction of an approximately 700 kb transcript map familial mediterranean fever locus on human chromosome 1 Genome Res. 9:1-21(1998).
-- PUNCTION: PUTATIVE ODORANT RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Centola M., Chen X., Sood R., Deng Z., Aksentijevich I., Bia Ricke D., Chen X., Wood G., Zaks N., Richards N., Krizman D. Mansfield E., Apostolou S., Liu J., Shafran N., Vedula A., H. Cercek A., Kahan T., Gumucio D., Callen D.F., Richards R.I., Moyzis R.K., Doggett N.A., Collins F.S., Liu P.P.,
                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00237; GPCRRHODOPSN. PRINTS; PR00245; OLFACTORYR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPRO00276; INTERPRO; IPRO00725; PFAM; PF00001; 7tm_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF098664; AAC83557.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           314 -- RNCMLTTLCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NESFVIYMFVVHFTIPLVIIFFCYGQLVFTVKEAAAQQQES-ATTQKAEKEVTRMVIIMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAFLICWVPYASVAFYIFTHQGSDFGPIFMTIPSFFAKSSSIY---NPVIYIMMNKQF--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLILILGNPKLKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7tm_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
  7 (POTENTIAL).
CYTOPLASMIC (P
BY SIMILARITY.
N-LINKED (GLCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
· ·) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krizman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ap around
> 16p13.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blake T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a collaboration - MBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hamon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o
o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
```

```
POSD_HUD
ACC POOD
TO DID
ACC POOD
TO DID
TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPSD_HUMAN STANDARD;
P08100; Q16414;
01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last seq
30-MAY-2000 (Rel. 39, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HOMO sapiens (Human).
Homo sapiens (Human).
'``rvota; Metazoa; Chordata;
'``rvota; Meraria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nathans J., Hogness
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE=84272729; PubMed=6589631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115
VARIANTS ADRP.
MEDLINE-91051574;
                                                                                                                      MEDLINE-90136922; PubMed-2137202;
Dryja T.P., McGee T.L., Reichei E.,
Yandell D.W., Sandberg M.A., Berson
                                                                                                                                                                                                                                                                                                                                                                                                Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rhodopsin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224
                                         Nature
[5]
                                                                                                                                                                                                                           "Rhodopsin mutations in autosomal Hum. Mutat. 2:249-255(1993).
                                                                                                                                                                                                                                                                     Al-Maghtheh M., Gregory Bhattacharya S.;
                                                                                                                                                                                                                                                                                                             MEDLINE-94004905; PubMed-8401533;
                                                                                                                                                                                                                                                                                                                                                                          Bennett J., Beller B., Sun D., Submitted (NOV-1994) to the EM
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85
                                                                                                                                                                                        VARIANT ADRP HIS-23.
                                                                                                                                                                                                                                                                                                                                   REVIEW ON ADRP VARIANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolation and nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
                                                                                                     "A point mutation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-----APLDLLLSCLAVSRIFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIFFIAILFSYLLTLLGNSTIILLSRLEARLHTPMYFFLSNLSSLDLAFATSSVPQMLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKEDTLAIQIFSFVAEF--SVPLLIFLFAVLLLIFS-LGRHTRQMRNTVAGSRVPGRGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIWLKMRISKLVPWM-----ILGSLLYVSMICVFHSKYAGFM--VPYFLRKFFSQNATI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LWGPGKTISYGGCITQLYV-FLWLGATECILLVVMAFDRYVAVCRPLRYTA----IMNPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LCWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FNTCLSHLLVVFLFYGSASYGYLLPAKNSKQDQGKFISLFYSLYT---PMVNPLIYTLRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q----AVLNGVCTFFTAVPLSIIVISYCLIAQAVLKIHSAE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEVKGALRRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PKLKQNAKKFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISALLSILSFLILYFSHCMIKVFL--SSLKFHIRRFIFLFFILVIGIYPSGHSLILILGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Natl.
                                                               343:364-366(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -IFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -LAVIAWLGGLGNSVIQSTFTLQLPLCGHRRVEGFLCEVPAMIKLACGDTSLN
                                                                                                                                                                                                                                                                                                                                                                                                                      1-120 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292
      PubMed=2239971;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1%;
                                                                                                         the rhodopsin
                                                                                                                                                                                                                                                                                             C., Inglehearn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence update) annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC4D7D349BE8B9E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81:4851-4855(1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                     Kariko K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123.5;
No. 0.
                                                                                                                                                                                                                                                        dominant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the
                                                                                                         gene
                                                                                                                               E.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348
                                                                                                                                                   Hahn L.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update
                                                                                                                                                                                                                                                                                                  :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .053;
                                                                                                             in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129;
                                                                                                             one
                                                                                                                                                                                                                                                                                                  Hardcastle A.,
                                                                                                                                                                                                                                                            retinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              encoding
                                                                                                                form
                                                                                                                                                     Cowley G.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                of
                                                                                                                                                                                                                                                          pigmentosa.";
                                                                                                                retinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
```

```
VARIANTS ADRP HIS-23; ARG-58; LEU-347 AN MEDLINE-91015273; PUbMed-2215617; Pryja T.P., McGer T.L., Hahn L.B., Cowle Reichel E., Sandberg M.A., Berson E.L.; "Mutations within the rhodopsin gene in dominant retinitis pigmentosa.", New Engl. J. Med. 323:1302-1307(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inglenear ...
Bhattacharva S.S.;
Bhattacharva S.S.;
a bp deletion in the rhodopsin g
and a bp deletion in the rhodopsin g
dominant retinitis pigmentosa.";
dominant retinitis pigmentosa.";
dominant retinitis pigmentosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Schinzel A., Samanns C., Gal A., Watty A., Ludwig M., Ludw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Farrar G.J., Kenna P., Redmond R., McWilliam !
Humphries M.M., Sharp E.M., Inglehearn C.F., !
Watty A., Ludwig M., Schinzel A., Samanns C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Europe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proline-->histidine substitution (codon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-91319709; PubMed-1862076; Sung C.H., Davenport C.M., Hennessey J.C., Maumenee I.H., Jacobson S.G., Heckenlively J.R., Nowakowski R., Fishman G., Gouras P., Nathans J.; "Rhodopsin mutations in autosomal dominant retinitis pigmentosa."; Proc. Natl. Acad. Sci. U.S.A. 88:6481-6485(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "pro-347-Arg mutation of the retinitis pigmentosa."; Genomics 11:468-470(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91090106; PubMed
Inglehearn C.F., Bashir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92021049; PubMed=1833777;
Dryja T.P., Hahn L.B., CowLey G.S., McGee T.L., E
"Mutation spectrum of the rhodopsin gene among pa
autosomal dominant retinitis pigmentosa.";
proc. Natl. Acad. Sci. U.S.A. 88:9370-9374(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gal A., Artlich A., Ludw.
Schwinger E., Schinzel A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92120672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT ADRP ARG-347.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT ADRP ILE-255 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS ADRP MET-17; HIS-23; ARG-58; SER-182 AND MEDLINE-91377732; PubMed-1897520; Sheffield V.C., Fishman G.A., Beck J.S., Kimura A. "Identification of novel rhodopsin mutations assoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS ADRP
                                                                                                                                                                                                                   Sharpe E., Humphries F.; "Autosomal dominant retinitis pigmentosa: rhodopsin gene in the original 3q linked fum. Mol. Genet. 1:769-771(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS ADRP
"Point mutations of rhodopsin gene found autosomal dominant retinitis pigmentosa (Jpn. J. Hum. Genet. 37:125-132(1992). [14]
                                                                                                                                                                                                                                                                                                                                                                                                                                         electrophoresis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                               retinitis pigmentosa by GC-clamped denaturing
                                                                                                             Fujiki K., Hotta Y.,
Sakuma T., Tamai M.,
                                                                                                                                                                                                                                                                                                                         Farrar G.J., Findlay J.B.C.,
                                                                                                                                                                                                                                                                                                                                               MEDLINE=93258325;
                                                                                                                                                                VARIANTS ADRP MET-17; AND LEU-347.
MEDLINE-93004784; PubMed-1391967;
                                                                                                                                                                                                                                                                                                                                                                        ARIANT ADRP ARG-207
                                                                                                                                                              MEDLINE=93004784;
                                                                                            Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genet. 47:941-945(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                        Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1840561;
.., Ludwig M., Niemeyer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=1985460;
                                                                                                                                                                                                                                                                                                                                                       PubMed=1302614;
                                                                                                                                                                                                                                                                                                                                                                                                                      49:699-706(1991).
                                                                                                                    Hayakawa M., Sakuma H., Shiono
Hikiji K., Kawaguchi R., Hoshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ×.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rhodopsin
                                                                                                                                                                                                                                                                                                                                   Kumar-Singh R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Beck J.S., Kimura A.E., Stone opsin mutations associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cowley G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND SER-347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                patients with autosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jay M., Bird A.C.
                                                     d in Japanese
(ADRP).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ы
                                                                                                                                                                                                                                                               family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01ek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P., Bradley D.G.,
Bashir R., Jay M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in autosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gal A.,
                                                                                                                                                                                                                                                                                                                                   Kenna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gradient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Olsson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEU-267
                                                                                                                                                                                                                                                                                                                                   ₽.,
                                                                                                                            A .
                                                                                  families with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           d with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Јау М.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              autosomal
                                                                                                                                                                                                                                                                                                                                      Humphries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dominant
                                                                                                                              Noro M.,
Nakajima A.,
                                                                                                                                                                                                                                                                                          in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E.M.,
                                                                                                                                                                                                                                                                                                                                          M.M.,
```

```
MEDLINE-95078858; PubMed-7987331; Souled E., Gerber S., Rozet J.M., Bonneau D., Du Philip N., Soubrane G., Coscas G., Munnich A.; "Five novel missense mutations of the rhodopsin dominant retinitis pigmentosa."; hum. Mol. Genet. 3:1433-1434(1994).
                                                                                  With
                                                                                                                                  VARIANTS ADRP ARG-40 AND LYS-216.
MEDLINE-94362717; PubMed-8081400;
Al-Maghtheh M., Inglehearn C., Lu
                                                                                                                                                                                                                                                                                                                                                                                                            Cabeza J.C.;
Cabeza J.C.;
"Identification of a new mutation at "Identification" at "Identificat
                VARIANT ADRP LEU-345
                                                                                                                       Bhattacharya S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antinolo G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT ADRP GLN-171.
MEDLINE-95078852; Pub
                                                                                                                                                                                                                                                                                                                                                       VARTANTS ADRP PHE-127; PRO-131; ASN-178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT CSNB4 GLU-292.

MEDLINE=93364423; PubMed=8358437;

Dryja T.P., Berson E.L., Rao V.R., Oprian "Heterozygous missense mutation in the rho congenital stationary night blindness.";

Nat. Genet. 4:280-283(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fuchs S., Kranich H., Denton M.J., Zrenno
Humphries P., Gal A.,
"Three novel rhodopsin mutations (CilOF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANTS ADRP PHE-110; PRO-131 AND VAL-164
MEDLINE-95072600; PubMed-7981701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of a novel rhodopsin mutation simplex case of retinitis pigmentosa."; Hum. Genet. 94:283-286(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94357587; PubMed-8076945; Reig C., Antich J., Gean E., Garc Carballo M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEDLINE-94375083; PubMed-8088850; Vaithinathan R., Berson E.L., Dryja "Further screening of the rhodopsin dominant retinitis pigmentosa."; Genomics 21:461-463(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Autosomal dominant 'sector' retinitis pigmentosa mutation predicting an Asn-15-Ser substitution of Hum. Mol. Genet. 2:813-814(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MacKe J.P., Davenport C.M., Jacobson S.G., Hennessey J.C. Gonzalez-Fernandez F., Conway B.P., Heckenlively J., Palm Maumenee I.H., Sieving P., Gouras P., Good W., Nathans J. "Identification of novel rhodopsin mutations responsible retinitis pigmentosa: implications for the structure and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT ADRP SER-15.
MEDLINE-93357759; Pu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS ADRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kranich H., Bartkowski
Duvigneau C., Gal A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        retinitis pigmentosa: implications rhodopsin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANTS ADRP A-51; I-104; R-106; G-135; S-140; E-188; M-209
MEDLINE-93304432; PubMed-8317502;
                                                  new rhodopsin transversion autosomal dominant retiniti Mutat. 3:409-410(1994).
                                                                                                                                                                                                                                                                                                                                                                                                     Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ູິJ. Hum. Genet. 53:80-89(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autosomal dominant retinitis pigmentosa."; Mol. Genet. 3:1203-1203(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADRP THR-44.
                                                                                                                                                                                                                                                                                                                                                                                                   Genet. 3:1421-1421(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8852; PubMed-7987326;
Sanchez B., Borrego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed=8353500;
owski S., Denton M.J.,
                                                                         retinitis pigmento
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Borrego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Garcia-Sandoval
                                                                                                                                       Lunt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s;
                                                                         pigmentosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zrenner E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                   pigmentosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                     codon 171 of rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rueda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rian D.D.;
rhodopsin
                                                                                                                                       Јау
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krey
                                                                                                                                                                                                                                                                                                                                                       ARG-267
                                                                         (L40R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in patients with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Т.,
                                                                                                                                    3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В.,
                                                                                                                                                                                                                                                                                                     Dufier J.L., Ghazi I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Met-44-Thr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chaparro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bhattacharya
                                                                                                                                    Bird
                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ly J., Palme
Nathans J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A164V) in
                                                                                           M216K) in
                                                                                                                                                                                                                                                                                                                                                     AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ramos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dickinson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     due to a point
rhodopsin.";
                                                                                                                                  .
                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                     ARG-297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Palmer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             c.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ayuso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s.s.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cause
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 β٦
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R-211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ō,
```

```
RESULT
OPSD_DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A Fasick J.I., Robinson P.R.;

L Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases,

1. FUNCTION: VISIAL PIGMENTS ARE THE LIGHT-ABSORBING MOLES

MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, OF LINKED TO CIS-RETINAL.

1. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

1. TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHILL

VISION IN DIM LIGHT.

2. IPTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RIBE PHOSPHORYLATED (BY SIMILARITY).

3. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPSD_DELDE
062791;
15-DEC-1998
15-DEC-1998
15-JUL-1999
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                              Delphinus delphis (Saddleback
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHODOPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94321123; PubMed=8045708;
Rosas D.J., Roman A.J., Weissbrod P., Macke J.P., Nathans "Autosomal dominant retinitis pigmentosa in a large family clinical and molecular genetic study.";
Invest. Ophthalmol. Vis. Sci. 35:3134-3144(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VARIANT ARRP LYS-150.
MEDLINE-95078913; PubMed-7987385;
Kumaramanickavel G., Maw M., Denton M.J.,
Orth U., Oehlmann R., Gal A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANT ADRP ALA-347.
MEDLINE-95359993; Puk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orth U., Oehlmann R., Gal A.;
"Missense rhodopsin mutation in a family with recessive Nat. Genet. 8:10-11(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39
                        OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMTIPAFFAKSAAIY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -NPVIYIMMNKQF----RNCMLTTICC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIDYYTLKPEVNNE---SFVIYMFVVHFTIPMIIIFFCYGQLVFTVKEAAAQQQES-ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----HPL----FIW---LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGENHAIMGVAFTWVMALACAAPPLAGW-----SRY----IPEGLQCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW-----LATWLGVFYCAKVASVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MLAAYM----FLLIVLGFPINFLTLYVTV------OHKKLRTPLNYILLNLAVADLFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 20.8
68; Conservative
                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37, 37, 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=7633434;
                                                                                                                                                                                                                                                                                                                                                                     Saddleback dolphin) (Black sea dolphin), Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Cetacea; Odontoceti; Delphin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last
Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 123.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s,
                                          COUPLED
                                                                                                                                 CELLS WHICH MEDIATES
                                                                                                                                                                                                    OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Srikumari C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tamily:
                                                                                    RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RΡ
                                                                                                                                                                                                                                                                                                                                                                Delphinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲
:.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
R
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
```

a collaboration - MBL outstation -

9

way

```
SOLUTION OF THE STATE OF THE ST
                                                                                                                                                                           Q
                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                      QΥ
                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                             οy
                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                        밁
                                                                                    Š
                                                                                                                                    밁
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00001; 7tm.1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1;
PROSITE; PS00238; GPROTEIN_RECEP_F1_2;
PROSITE; PS00238; OPSIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
DISULFID
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF055314; AAC12761.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIPID
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                  155
                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                                                                                                         97
                                                                                                                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                                                                                                                                                  45
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 FLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQLFIFYVNVI 68
                                                                                                                                                                                                                                                                                                                                                               VIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR----HPLFI 116
                                                                                                                                                                               OKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISA 226
                                                                                                                                                                                                                                                                        WLKMRISKLVPWMILGSLLYVSMIC-----VFHSKYAGFMVPYFLR-----KFFSQNATI 166
                                                                                                                                                                                                                                                                                                                      TSLHAYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFRFGENHAI-- 154
                                                                                                                                                                                                                                                                                                                                                                                                               FLLIVLGFPINFLTLYVTV------OHKKLRTPLNYILLNLAVANLFMVFGGFTTTLY 96
    KLKQNAKKFLLHSKCC
                                             IIMVVAFLICWVPYASVAFYIFTHQGSDFGPIFMTIPSFFAKSSSIY----NPVIYIMMNK 311
                                                                                                                                                                                                                                ----MGLALTWI-----MAMACAAPPLVGWSRY----IPEGMQCSCGIDYYTLSPEV
                                                                                         LLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLILILGNP
                                                                                                                                    NNE---SFVIYMEVVHFTIPLVIIFFCYGQLVFTVKEAAAQQQES-ATTQKAEKEVTRMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000276;
IPR000732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   343
348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
37
62
74
99
114
1134
153
177
203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110
110
296
322
323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retinal protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.1%;
       298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΜW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (POTENTIAL).
EXTRACELLULAR.
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 (POTENTIÂL).
CYTOPLASMIC.
ACETYLASTICN (BY SIMILARITY)
ACETYLATION (BY SIMILARITY)
N-LINKED (GLCNAC. . .) (BY :
N-LINKED (GLCNAC. . . ) (BY :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR.
7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 (POTENTIAL).
CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR
3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 123; DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PHOSPHORYLATION (BY RK) (BY SIMILARITY).
70D8663DF7F59080 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
RETINAL CHROMOPHORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Palmitate; G-protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane; Glycoprotein; Vision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                  254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
```

```
RESULT 13
GP41_HUMAN
ID GP41_H
AC 014843
AC 014843
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT 15-JUL
DT SEQUEN
RN (1]
RN (1]
RP SEQUEN
RX MEDLIN
RA O'DOWG
RT "A CIL
RT OCCULT
CC -!- SI
CC -!- SI
CC -!- SI
CC This !
CC This !
CC This !
CC This !
CC The B
CC Lhe B
CC This !
CC This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            멍
                       Ş
                                                                                   망
                                                                                                                                   ρ
                                                                                                                                                                                           Query Match
Best Local S
Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCRDB; C
GCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUL-1999 (Rel. 38, Last annotation update) PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GP41_HUMAN 
014843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a class the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O'Dowd B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sawzdargo M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98008875; PubMed=9344866;
                                                                                                                                                                                                                                                                                                                                       CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; G_PROTEIN_RECEP_F1_1; Transmembrar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF024688; AAB86711.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          occurring in close
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A cluster of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                18
                                                                                                                                         10
                             70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QF ---- RNCMLTTLCC
                                                                                FSVYLLTELVGLPLN-LLALVVFVGKLQRRPVA-VDVLLLNLTASDLLLLLELPFRMVEA 75
                                                                                                                                      FLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIV
I----FFIEFTMCSANCAILLEINELELWLATWLGVFYCAKVASVRHPLFIWLKMR----
                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR000276;
                                                                                                                                                                                                                                                                                                                                                                                                102
102
103
1133
1133
1154
1179
1179
1200
223
2244
2244
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          four novel human G protein-coupled receptor close proximity to CD22 gene on chromosome 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                George
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7tm_1;
                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                     40
47
68
80
101
132
153
178
178
199
222
222
243
2543
2543
                                                                                                                                                                                                                                                                                                                                             38649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.R., Nguyen
                                                                                                                                                                                                                               8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ximity to CD22 gene on chro
Commun. 239:543-547(1997).
                                                                                                                                                                                                                                                                                                                                                   X
X
                                                                                                                                                                                                          53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane.
                                                                                                                                                                                                                               Score 122.5; DE Pred. No. 0.067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (P
B3B19D62D11B6BA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      7 (POTENTIAL)
CYTOPLASMIC (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 (POTENTIAL)
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xu S., Kolakowski L.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 19q13.1.";
                                                                                                                                                                                                          93;
                                                                                                                                                                                                                                                                Length 346;
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration -
MBL outstation -
                                                                                                                                                                                                                79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outstation
                                                                                                                                                                                                             Gaps
                                               121
                                                                                                                                                          69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        o
                                                                                                                                                                                                                18;
```

```
THE THE TRANSPORT OF THE TRANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
OPSD_PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
    TRANSMEM
DOMAIN
                                               TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPSD_PHOVI
062794;
15-DEC-1998
15-DEC-1998
15-JUL-1999
                                                                                                                                                                                                                                                            PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; PROSITE; PS00238; OPSIN; 1
                                                                                           DOMAIN
                                                                                                              TRANSMEM
                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                           PRINTS; PR00237; GPCRRHODOPSN
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
                                                                                                                                                           TRANSMEM
                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                     Acetylation
                                                                                                                                                                                                                           Phosphorylation;
                                                                                                                                                                                                                                                  Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF055317; AAC12764.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FBSick J.I., Robinson P.R.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT
- MEDIATE VISION. THEY CONSIST OF AN APOPROTEIN, OPSIN, COVALENTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPRO00276; -. INTERPRO; IPRO00732; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RHO
                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phoca vitulina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LAOHd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LINKED TO CIS-RETINAL.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIAT VISION IN DIM LIGHT.
PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES M BE PHOSPHORYLATED (BY SIMILARITY).
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPSIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAGLLAATLLNFLVCFGPYNVSHVVGYICGESPAWRIYVTLLSTLNSCVDPFVYYF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TLAI----QIFSFVAEFSVPLLIFLFAVLLLIFSLGR---HTRQMRNTVAGSRVPGRGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLAILLPVRLEMAVVLEVVPLIITSYCYSRLVWILGRGGSHRRQRR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QAGLVSVACWLLASAHCSVVYVIEFSGDISHSQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---ISKLVPWMILG---SLLYVSMIC--VFHSKYAGFMVPYFLRKFFSQNATIQ---KED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANGMHWPLPFTLCPLSG--FIFFTTIYL-TALFLAAVSIERFLSVAHPL--WYKTRPRLG
                                                                                                                                                                                                                                                                                                                                                                                                                            IPR001760
    1
37
62
74
99
114
134
153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 37, Created)
(Rel. 37, Last sequence up)
(Rel. 38, Last annotation
                                                                                                                                                                                                                                                  Retinal
                                                                                                                                                                                                                                                                                                                                                                                                       7tm_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Harbor seal).
azoa; Chordata; (eria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                    Lipoprotein;
    36
61
73
98
113
113
152
176
                                                                                                                                                                                                                                                protein;
                     1 (POTENTIAL).
CYTOPLASMIC.
2 (POTENTIAL).
EXTRACELLULAR.
3 (POTENTIAL).
CYTOPLASMIC.
4 (POTENTIAL).
EXTRACELLULAR
                                                                                                                                                                           EXTRACELLULAR
                                                                                                                                                                                                                    Palmitate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Pinnipedia; Phocidae; Phoca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions ong as its content is in
                                                                                                                                                                                                                    G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                               Glycoprotein; Vision;
tein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELLS WHICH MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -GTNGTCYLEFRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₩ay
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
REDLINE-9747534; Pubmed-9335046;

X MEDLINE-9747534; Pubmed-9335046;

XA Petters R.M., Alexander C.A., Wells K.D., Collins E.B., Sommer J.R.,

XA Petters R.M., Alexander C.A., Wells K.D., Collins E.B., Sommer J.R.,

XA Cladeciyan A.V., Jacobson S.G., Wong F.;

XT. "Genetically engineered large animal model for studying cone

yhotoreceptor survival and degeneration in retinitis pigmentosa.";

XI. Nat. Biotechnol. 15:965-970(1997).

XI. NAT. BIOTECTION: VISUAL PIGMENTS ARE THE LIGHT-ABSORBING MOLECULES THAT

MEDLINED TO CIS-RETINAL.

XI. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

XI. SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

XI. TISSUE SPECIFICITY: ROD SHAPED PHOTORECEPTOR CELLS WHICH MEDIATES

XI. VISION IN DIM LIGHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 65
                                                                                                                                                                                                          RHO OR RHO1.
Sus scrofa (Pig).
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                               15-JUL-1998
15-JUL-1998
15-JUL-1999
                                                                                                                                                                                                                                                                                                       OPSD_PIG
018766;
                                                                                                                                                                                                                                                                                                                                   PIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIPID
MOD_RES
SEQUENCE
                                                                                                                                                                                                  Mammalia;
                                                                                                                                                                                                                                                     RHODOPSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
CARBOHYD
CARBOHYD
DISULFID
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIPID
                                                                                                                                                                                                                                                                                                                                                                                     302
                                                                                                                                                                                                                                                                                                                                                                                                              272
                                                                                                                                                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
                                                                                                                                                                                                                                                                                                                                                15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLESHLIIYELLAVIQELLGIFTNGIIYVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ
                                                                                                                                                                                                                                                                                                                                                                                 -NPVIYIMMNKQF----RTCMITTLCC
                                                                                                                                                                                                                                                                                                                                                                                                          GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                QKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMTLPAFFAKAASIY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GIDYYTLKPEVNNE---SFVIYMFVVHFTIPMIVIFFCYGQLVFTVKEAAAQQQES-ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -- KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----HPL----FIW----LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MLAAYM---FLLIVLGFPINFLTLYVTV------QHKKLRTPLNYILLNLAVADLFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGENHAIMGVGFTWVMALACAAPPLVGW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Similarity
65; Conser
                                                                                                                                                                                                  Eutheria;
                                                                                                                                                                                                                                                            (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
110
296
322
323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.
                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
2
187
187
296
322
323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.1%;
19.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38973 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC...) (BY SIMILARITY).
N-LINKED (GLCNAC...) (BY SIMILARITY).
BY SIMILARITY.
RETINAL CHROMODHORE.
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PALMITATE (BY SIMILARITY).
PHOSPHORYLATION (BY RK) (BY SIMILARITY).
B51B9CBDBCEEFBE8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 (POTENTIAL).
CYTOPLASMIC.
6 (POTENTIAL).
EXTRACELLULAR.
7 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 122.5; DB 1;
Pred. No. 0.067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 (POTENTIAL).
CYTOPLASMIC.
ACETYLATION (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          298
                                                                                                                                                                                                                                                                                                                  348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----SRY----IPEGMQCSC
                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71;
             MEDIATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
```

```
THE TEXT OF A PART OF A PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9,
                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         οy
                                                                                                        Вþ
                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                       밁
                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no we use by non-profit institutions as long as its content is in no we use by non-profit institutions as long as its content is in no we use by non-profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we use the profit institutions as long as its content is in no we are the profit institutions as long as its content is in no we are the profit institutions as long as its content is in no we are the profit institutions as long as its content is in the profit institution as long as its content is in the profit institution as long as its content is in the profit institution as long as its content is in the profit institution as long as its content in the profit institution as long as its content in the profit institution as long as its content in the profit institution as long as its content in the profit institution as long as its content in the profit institution as long as its content in the profit institution as long as its content in the profit institution as long as its content in the profit instit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCRDB; GCR_2564;
INTERPRO; IPR000276;
INTERPRO; IPR000732;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00237; GPCRRHODOPSN.
PRINTS; PR00238; OPSIN.
PRINTS; PR00579; RHODOPSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO; IPR001760; -. PFAM; PF00001; 7tm_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF008947; AAB86808.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acetylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
                                      158
                                                                                                            148
                                                                                                                                                                                      112
                                                                                                                                                                                                                                                                                                                                 60
                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                       39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: SOME OR ALL OF THE CARBOXYL-TERMINAL SER OR THE RESIDUES PATE BE PHOSPHORYLATED.

BE PHOSPHORUS: THIS RHODOPSIN HAS AN ABSORPTION MAXIMA AT 495 NM. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLESHLIIYELLAVIQELLGIETNGIIVVVNGIDLIKHRKM-APLDLLLLSCLAVSRIELQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPSIN SUBFAMILY
                                                                                                                                                                                                                                                                                                                             LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                       FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR 147
                                                                                                                                                                                                                                                                                                                                                                                                           MLAAYM---FMLIVLGFPINFLTLYVTV-----
--KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS
                                                                                                        FGENHAIMGLALTWVMALACAAPPLVGW------SRY----IPEGLQCSC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; PS50262; ; PS00238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PS00237; G_PROTEIN_RECEP_F1_1; 1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
                                                                                                                                                                  -HPL----FIW----LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
15
96
296
322
323
183
343
343
39027 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Retinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stinal protein; Transmembrane; Glycoprotein; Vision; Lipoprotein; Palmitate; G-protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPSIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36
61
73
98
113
113
152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF THE CARBOXYL-TERMINAL SER OR THR RESIDUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACEMENT OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 122.5; DB 1;
Pred. No. 0.067;
2; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 (POTENTIAL).
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PALMITATE.
PALMITATE.
BY SIMILARITY.
PHOSPHORYLATION (BY RK) (BY SIMILARITY).
; 272E6B0BEE3DA51B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                               -QHKKLRTPLNYILLNLAVADLFMV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration -
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAY
                                                          215
                                                                                                                                                                                                     157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
```

Search completed: March 15, 2001, 13:20:35 Job time: 1355 sec

```
Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŏ
18
19
20
21
22
23
24
25
26
27
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
131
130.5
129.5
128.5
125.5
124.5
124.5
122.5
122.5
122.5
122.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
121.5
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR_66:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MLESHLIIYFLLAVIQFLLG......GNPKLKQNAKKFLLHSKCCQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-510-332-1
1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195891 seqs, 67900655 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                            Length DB
  OOSH

S231677

T26188

E22845

D58931

D58931

IG1746

JC5715

JC5715

JC5715

I51319

A70201

JC5720

A31318

A45229

JW0120

A3131866

A45229

A3131866

S689366

S68936

OSB932

OOB9

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JC4267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S52960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195891
                                                                               G protein-coupled opsin, green sensi rhodopsin, green sensi rhodopsin - Japane glucose transporte Mel-1c receptor su glucose transport glucose transport NADH dehydrogenase angiotensin II rec cytochrome C-type rhodopsin - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical prote
hypothetical prote
NADH dehydrogenase
rhodopsin - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pheromone receptor G protein-coupled hypothetical prote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rnodopsin - sheep
rhodopsin - Chines
rhodopsin - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opsin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                                                                                                                                                                                                                           opsin - mouse
RH2 opsin - gi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADH dehydrogenase
                                                             rhodopsin - green
                                                                                                                                                                                                                                                                                                                                                                                                       virulence factor m
        opsin,
                                      opsin,
           green-sensi
rod - dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rabbit
                                                                                                                                                                                                                                                                                                                                                                                                                              green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - honeybee mitochondric C;Species: mitochondrion Apis mellifera (honeybee) A;Variety: liqustica A;Variety: liqustica C;Bate: 28-Oct-1996 *sequence_revision 13-Mar-1997 *text_change 17-Mar-2000 C;Bate: 52960 C;Accession: $52960 R;Crozier, R.H.; Crozier, Y.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
S52960
```

45	44	43	4 2		4	40	39	S) (۲ 7	ω 6	Ü	n n	ω A	(a	, (2	ů.) ر ا د	0		
111	111.5	111.5	111.0		111.5	111.5	111.5	717	ן <u>ר</u>	112	112	TTO	2	113.5	114	1 1	114	T.#. J	7	115	,	
7.3	7.3	7.3		ا د	7.3	7.3	7.3		7	7.4	7.4	. ;	л	7.5		J J	7.5		J J	. 0	,	
274	468	900	1 (350	355	354	2/4	1 6	л Э	320	269) (ر م	345		770	262		725	000	200	
٨.	N	۸ ا) 6	J	_	۰) 1	s	N	٨) ;	N	-		ں	N) }	_	1	د	
S4 2168	A/2619	A4 2000		101194	A46191	52/231	211777	200	506920	S20573	D/0404	1000	JC1104	MMBET /		672589	8/0658	1	151200	FOLICE	257100	
March	יייי פייי	210	. and	angı	Touc	1000	7,00	NADH	gluc	, 1	3.5	hypo	angı		38.	nypo	, (011)	COnc	rnoa		dora	
in dental and dental a	JADH dehydrogenase		andiotensin II rec	angiotensin ii rec		and a homolog -	hodonsin - northe	ADH dehydrogenase	lucose transport	Traccot I reaches	otory recentor	vnothetical prote	and to censui it iec	otongin II rec	a ik membrane pro	nypothetical proce	Chick in Found	conserved hypothet	logopsin - write		probable iron-upta	

ALIGNMENTS

honeybee mitochondrion

										_						_				
дд	Qy	Db	ОУ	Db	Qy	Db	Qу	Db.	Qy	Db	Qy	Quer Best Matc	C; Super C; Keywo	A; Genon A; Genet	C;Genetics:	A; Resid	A;Statu A;Molec	A; Acces	A;Title	R;Crozi
278 LMIWNYIIILKRYFLKMNFYKNNFIDDKDNKYMYHS 313	270 PSGHSLILIIGNPKLKQNAKKFLLHS 295	228YQMYTELTLMENYSMYPIFLSFVIKWNLIFMMVSVKAYNWILFLLMISSM 277	218 PGRGAPISALLSTLILYFSHCMIKVFLSSLKFHIRRFIFLFFILVIGIY 269	169 KKLLACSTIENSFYFIFILELNKNMFIAMIILYSFNYFLLISFLNKF	163 NATIQKEDTLAIQIFSEVAEESVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRV 217	125 MSTLIKE-IPIYMMVSMTKINSWTLYFLITNSLYIS	104 CAKVASVRHPLFIWLKM-RISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLRKFFSQ 162	66 SSIFL-FFMIIVYLSSISETKTDTFNFMVQMMFFLKIGTFPFHFWMI	54 SRIFLQLEIFYVNVIVIFEIEFIMCSANCAILLFINELELWLATWLGVFY 103	9 HWFIYFLITIFVLMMNSNNIFIQWMLMEFGTIISISLIN-IKSTNKTPSLIYYSVSVI 65	5 HLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAV 53	Query Match 8.6%; Score 131; DB 2; Length 333; Best Local Similarity 19.9%; Pred. No. 0.001; Matches 67; Conservative 63; Mismatches 130; Indels 76; Gaps	C; Superfamily: NADH denyurogenase (uniquinous) control N. C; Keywords: membrane-associated complex; mitochondrion; N.	A; Genetic code: SGC4 A; Genetic code: SGC4	etics:	A;Residues: 1-333 <cro></cro>	A;Status: preliminary A:Molecule type: DNA	A; Reference number. Subsection in the second subsection in Second subsection in Second subsection in the second subsecti	A;Title: The mitochondrial genome of the honeybee Apis mellifera:	R;Crozier, R.H.; Crozier, I.C.
		NYNWILFLLMISSM 277	REIFLEFILVIGIY 269	NIQNENEMEYNK- 22/	TROMENTVAGSEV 217	FYANKFYTL 168	EMVPYFLRKFFSQ 162	YSYEMMNWKQIFL 124	LATWLGVFY 103	KTPSLIYYSVSVI 65	MAPIDILLSCLAV 53	th 333; dels 76; Gaps 13;	NAD; oxidoreductase						lifera: complete sequence	

```
rhodopsin - sheep (Species: Ovis orientalis aries, Ovis ammon aries (domestic) Species: Ovis orientalis aries, Ovis ammon aries (domestic) Date: 18-Aug-1982 #sequence_revision 30-sep-1990 #text_chcc: Accession: A30407; A90319; A93264; A03155 R; Pappin, D.J.C.; Elipoulos, E.; Brett, M.; Findlay, J.B.C. Int. J. Biol. Macromol. 6, 73-76, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;109-133/Domain: transmembrane *status predicted CTM3>
F;152-176/Domain: transmembrane *status predicted CTM4>
F;103-127/Domain: transmembrane *status predicted CTM5>
F;253-277/Domain: transmembrane *status predicted CTM5>
F;253-277/Domain: transmembrane *status predicted CTM5>
F;266-310/Domain: transmembrane *status predicted CTM7>
F;215/Binding site: carbohydrate (Asn) (covalent) *status predicted F;110-187/Disulfide bonds: *status predicted F;110-187/Disulfide bonds: *status predicted F;295/Binding site: palmitate (Cys) (covalent) *status predicted F;295/Binding site: phosphate (Ser) (covalent) (by rhodopsin F;334,338,347/Binding site: phosphate (Thr) (covalent) (by rhodopsin F;336,340,342/Binding site: phosphate (Thr) (covalent) (by rhodopsin F;336,340,342/Binding site: phosphate (Thr) (covalent) (by rhodopsin F;336,340,342/Binding site: phosphate (Thr) (covalent)
                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Cross-references: GB:U21688; NID:9710429; PIDN:AAA91640.1; A:Accession: PC4072
A:Molecule type: protein
A:Residues: 1-39;318-348 <SM2>
A:Experimental source: rod photoreceptor cells
C:Comment: This protein is a component of rhodopsin together
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  opsin - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: JC4267; pC4072
R;Smlth, W.C.; Martinko, J.M.; Wheeler, J.N.; Hargrave, P.A.; McDowell, J.H.
Gene 162, 331-332, 1995
A;Title: The deduced amino-acid sequence of opsin from rabbit rod photoreceptors.
A;Reference number: JC4267; MUID:96032368
A;Accession: JC4267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: vertebrate rhodopsin
C;Keywords: chromoprotein; eye; G protein-coupled recep;37-61/Domain: transmembrane #status predicted <TM1>F;75-99/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-348 <SMI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                     307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162 QNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 NESFY-----IYMFVVHFTIPLIIIFFCYGQLVFTVKEAAAQQQES-ATTQKAEKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 21.8 es 70; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                                                                                                                                                                                                                               ILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                      VTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMTIPAFFAKSSSIY---NPVIY
                                                                                                                                                                                                                                                                                                                                                                                                  APISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGENHAIMGVAFTWI-MALACAAP-PLVGWSRYIPEGMQCSCGIDY-----YTLKPEVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----HPL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGGFTTTLYTSLHGYFVFGPTGCNVEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLAAYM---FLLIVLGFPINFLTLYVTV------QHKKLRTPLNYILLNLAVADLFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.6%;
                                                                                                                                                                                                                                                                                                               298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G protein-coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 130.5; DB Pred. No. 0.0012; 4; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rhodopsin together with the retinoid chromopho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128;
                                                                              #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycoprotein; lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID: 9710430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kinase) #status
kinase) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
                                                                                                                                                                                                                                                                                                                                                                                                                                                       249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pro
                                                                 Ş
                                                                                                                        밁
                                                                                                                                                                       S
                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                              216 RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL---
                                                                                                                          188
                                                                                                                                                                                                                         148
                                                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                                                                                                                                                                          39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
               QKAEKEVTRMVIIMVIAFLICWLPYAGVAFYIFTHQGSDFGPIFMTIPAFFAKSSSVY--
                                                                                                           GALYFTLKPEINNE---SFVIYMFVVHFSIPLIVIFFCYGQLVFTVKEAAAQQQES-ATT
                                                                                                                                                     --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGS
                                                                                                                                                                                                                   FGENHAIMGVAFTWVMALACAAPPLVGW---
                                                                                                                                                                                                                                                             ----HPL----FIW----LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                                                                            FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
                                                                                                                                                                                                                                                                                                                                                         LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                MLAAYM---FILIVLGFPINFLTLYVTV-----QHKKLRTPLNYILLNLAVADLFMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-348 <PAP>
```

187 157 147 87

243

```
F;114-133/Domain: transmembrane #status predicted <TMM>
F;53-175/Domain: transmembrane #status predicted <TMM4>
F;203-230/Domain: transmembrane #status predicted <TMM5>
F;203-276/Domain: transmembrane #status predicted <TMM5>
F;233-276/Domain: transmembrane #status predicted <TMM5>
F;285-309/Domain: transmembrane #status predicted <TMM7>
F;1/Modified site: acetylated amino end (Met) #status experimental
F;2.15/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;296/Binding site: retinal (Lys) (covalent) #status experimental
F;322,323/Binding site: palmitate (Cys) (covalent) #status predicted
F;334,338,343/Binding site: phosphate (Ser) (covalent) (by rhodopsin kinase) #status
F;335,336/Binding site: phosphate (Thr) (covalent) (by rhodopsin kinase) #status expe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A33264; MUID:82013638
A; Accession: A33264; Findlay, J.B.C.
A; Residues: 240-348 <FIN>
A; Residues: 240-348 <FIN
A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;37-61/Domain: transmembrane #status predicted <TM1>F;74-96/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: acetylated amino end; chromoprotein; eye; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1;40-44;45-86;87-111;144-155;156-163;164-183;184-207;208-241 <BRE>
R; Findlay, J.B.C.; Brett, M.; Pappin, D.J.C.
Nature 293, 314-316, 1981
A; Title: Primary structure of C-terminal functional sites in ovine rhodopsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochem. J. 211, 661-670, 1983
A; Title: Isolation and characterization of the
A; Reference number: A90319; MUID:83282605
A; Accession: A90319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A:Note: no explanation is given f
A:Note: peptides and unsequenced
R:Brett, M.; Findlay, J.B.C.
Biochem. J. 211, 661-670, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: A structural model A;Reference number: A91755 A;Accession: A30407
1 MLESHLIIYFLLAVIQFFLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                                                                                  Conservative
                                                                                                                                                                                            8.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for ovine rhodopsin
                                                                                                                                             62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for the did
                                                                                                                                                                                            Score 129.5; DB Pred. No. 0.0014;
                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       differences in the sequence as es are ordered by homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNBr peptides
                                                                                                                                                                                                                                      DB 1;
                                                                                                                                             125;
                                                                                                                                        Indels
                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from the proteolytically
                                                                                                                                        71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mammalian rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seen ir
                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rhodops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sit
```

```
C;Species: Cricetulus griseus (Chinese C;Date: 10-Sep-1999 #sequence_revision C;Accession: S23398 R;Gale, J.M.; Tobey, R.A.; D'Anna, J.A. J. Mol. Biol. 224, 343-358, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: vertebrate rhodopsin
C; Keywords: chromoprotein: eye; G protein-coupled receptor;
F; 37-61/Domain: transmembrane #status predicted <TM1>
F; 74-96/Domain: transmembrane #status predicted <TM2>
F; 114-133/Domain: transmembrane #status predicted <TM4>
F; 115-175/Domain: transmembrane #status predicted <TM4>
F; 153-175/Domain: transmembrane #status predicted <TM5>
F; 253-276/Domain: transmembrane #status predicted <TM5>
F; 285-399/Domain: transmembrane #status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Localization and DNA sequence of a A;Reference number: S23398; MUID:92219256 A;Accession: S23398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X61084; NID:g49478; PIDN:CAA43398.1; PID:g49479 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-348 <GAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rhodopsin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Introns: 121/1; 177/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
9
                                                                                                                                                                                                                            RESULT
S51677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                  rhodopsin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :296/Binding site: retinal (Lys) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162
                                                                                                                                                                                                                                                                                                                                              307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NPVIYIMMNKQF----RNCMLTTLCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVICKPMSNFR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VTRMVILMVVFFLICWFPYAGVAFYIFTHQGSNFGPIFMTLPAFFAKSSSIY---NPVIY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRG 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----HPL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFS 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLIL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NESFV-----IYMFVVHFTIPLIVIFFCYGQLVFTVKEAAAQQQES-ATTQKAEKE 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FGENHAIMGVVFTWI-MALACAAP-PLVGWSRYIPEGMQCSCGVDY-----YTLKPEVN
                                                                                                                                                                                                                                                                                                                                                                                                       ILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chinese hamster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
                                                                                                                                                                                                                                                                                                                                                                                                       298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 128.5; DB 1;
Pred. No. 0.0017;
3; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hamster)
10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             replication origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein; lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the rhodopsin
                                            opsin mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                               in
                                               albin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                       밁
```

```
A;Molecule type: mRNA
A;Residues: 1-348 <-HUB>
A;Residues: 1-348 <-HUB>
A;Cross-references: EMBL:Z46957; NID:g603874; PIDN:CAA87081.1; PID:g603875
A;Cross-references: EMBL:Z46957; NID:g603874; PIDN:CAA87081.1; PID:g603875
C;Superfamily: vertbbrate rhodopsin
C;Keywords: chromoprotein; eye; G protein-coupled receptor; lipoprotein; pi
C;Keywords: chromoprotein (Lys) (covalent) #status predicted
F;296/Binding site: retinal (Lys) (covalent) #status predicted
F;322,323/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: S51677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Caenorhabditis elegans
C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein W05B5.2 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data A; Reference number: Z20167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T26188
                                                                                                                                                                                                                                                              A;Map position: 1
A;Introns: 48/2; 97/3; 146/3; 185/1;
C;Superfamily: neurokinin 1 receptor
                                                                                                                                                                                                                                                                                                                                              A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-382 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; McLay, K.
                                    γg
                                                                             밁
                                                                                                                ρy
                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: Z82071; PA: Experimental source: clone W05B5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number:
A; Accession: T26188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                         веst Local
Matches б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                 Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 MLAAYM---FILIVLGFPINFLTLYVTV-----QHKKLRTPLNYILLNLAVADLFMV
  108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ
                                      51 LAVSRIFLQLFIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFY-CAKVAS 109
                                                                                  50
                                                                                                                           æ
                                                                                                                                                                                                                                                                                                                             CESP:W05B5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKAEKEVTRMVIIMVIFFLICWLPYASVAMYIFTHQGSNFGPIFMTLPAFFAKTASIY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIDYYTLKPEVNNE---SFVIYMFVVHFTIPMIVIFFCYGQLVFTVKEAAAQQQES-ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----HPL----FIW---LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIGLWSLVVLAIERYVVVCKPMSNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHSLILILGNPKLKQNAKKFLLHSKCC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FGENHAIMGVAFTWVMALACAAPPLVGW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NPITYIMMNKQF----RNCMLTTLCC
LAIADLLILLECLPLTVVNDVTKTFWFSAVFCKSVNFVNNTSVYVSIMSLVFITCERWRA 167
                                                                               VYILASMM--VIGVIGNTLVVVVVATNKSMVGRMGTGNRGNRVVCSMFHKRNALNLVLMN 107
                                                                                                                      IYFLLAVIQFLLGIFTNGIIVVV------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66;
                                                                                                                                                             l Similarity
60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                        clone
                                                                                                                                                                                   8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 125.5; DE Pred. No. 0.003;
                                                                                                                                                                                                                                                                                                                                                                                            PIDN:CAB04918.1;
                                                                                                                                                                                   Score 125; DB 2;
Pred. No. 0.0035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     November
                                                                                                                                                                    Mismatches 105;
                                                                                                                                                                                                                                                                                        216/3; 268/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              323
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB/EMBL/DDBJ
                                                                                                                             ----NGIDLIKHRKMAPLDLLLSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----SRY----IPEGMQCSC
                                                                                                                                                                                                                                                                                                                                                                                                GSPDB:GN00019; CESP:W05B5.2
                                                                                                                                                                                                           Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 348;
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-Jun-2000
                                                                                                                                                                        60;
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187
                                                                                                                                   50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphoprote
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
                                                                                                                                                                          11;
```

```
A; Title:
                                     NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 2 - Cyanidioschyzon merolae C;Species: mitochondrion Cyanidioschyzon merolae C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 20-Jun-2000 C;Accession: D59931
R;Ohta, N.; Sato, N.; Kuroiwa, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 7
E22845
Figure 7
RESULT 7
RE2845
Appothetical protein 4 - Trypanosoma brucei mitochondrion C;Species: mitochondrion Trypanosoma brucei
C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_
C:Accession: E22845
C:Accession: E27845
                                                                                                                                                                                                                  Š
                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                               Ъ
                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                       õ
                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: hypothetica C; Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Genetic code: SGC6
C;Superfamily: hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Hensgens, L.A.M.; Brakenhoff, J.; De Vries, B.F.; Sloof, P.; Tromp, M.C.; Van Boom, J. Nucleic Acids Res. 12, 7327-7344, 1984
A:Title: The sequence of the gene for cytochrome c oxidase subunit I, a frameshift conta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Genome: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-445 <HEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A93537; MUID:85037915
A;Accession: E22845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                      315
                                                                                                                                                                                                                  282 PKLKQNAKKFLLH 294
                                                                                                                                                                                                                                                                                    227
                                                                                                                                                                                                                                                                                                                  222
                                                                                                                                                                                                                                                                                                                                                 169
                                                                                                                                                                                                                                                                                                                                                                                 181
                                                                                                                                                                                                                                                                                                                                                                                       110 VRHPLEIWLKMRISKLVPWMILGSLLYVSM-ICVEHSKYAGEMVPYFLRKFESQNATIQK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                              134
 N.; Sato, N.; Kuroiwa, T. Acids Res. 26, 5190-5198, 1998 acids res. 26 organization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 QISIRKKAVRMLCAV----VFLFS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                       8
                                                                                                                                                                                     FDFKYNENYFLIN
                                                                                                                                                                                                                                         LLEVLSVNNECELELIFISTKNYIFYLYLNEHLIYSISLVLLIII------YYFFIIYNI
                                                                                                                                                                                                                                                                      LLSILS-----FLILYFSHCMIKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILILGN
                                                                                                                                                                                                                                                                                                        --ILIILLISFIYFYILFIKLLLFQSCTCVLI-----GLNSFA-----IVS
                                                                                                                                                                                                                                                                                                                            EDTLAIQIFSEVAEF--SVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISA
                                                                                                                                                                                                                                                                                                                                                                                                                                  YYMLNLINFILLFILLYFMILNYCFFLCDFCFLVFDEE-----WLGILCLFY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                FY----VNVIVIFFIEFIMCSANC-----AILLFINELELWLATWLGV---FYCAKVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIIIIIQYIIIFLFIFINHIIIISILFEI-----FSLLLFLLLMSSRFGYKILVLMY 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLLAVIOFL----LGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIF----LQLFI 62
                                                                                                                                                                                                                                                                                                                                                                       ---TLLILEKLYIAFLILEM---EQLYIRLGVFIFI----YMLTEYILFCF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHI 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----FSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRCKESWSEEFQKNYQLLQTIFSFV----LPLLVISILCLHMVRTL--HFSANYLTVANR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITYPLKSPFVRTR------SVIGGIWFIAMFLSSPEPVTLHLAGAPFVRPNPTTKWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein 1 (CYb-COII intergenic region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 124.5; DB Pred. No. 0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M1smatches
   the mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -MSNLPVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 445;
   genome
 of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95;
the unicellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                         281
                                                                                                                                                                                                                                                                                                                                        226
                                                                                                                                                                                                                                                                                                          260
                                                                                                                                                                                                                                                                                                                                                                       221
                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                           mitochon
red
                                                                                                                                                                                                                                                                                                                                                                                                                                                               р
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÔ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
```

```
A;Reference number: A58930; MUID
A;Accession: D58931
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-500 <ARN>
A;Cross-references: GB:D89861; N
C;Genetics:
A;Gene: nad2
R; Inglehearn, C.F.; Bashir, R
Am. J. Hum. Genet. 48, 26-30,
A; Title: A 3-bp deletion in the
A; Reference number: A36537; M
A; Accession: A36537
                                                                                     hattacharya, S.; Humphries, P.
Am. J. Hum. Genet. 47, 941-945, 1990
A;Title: Autosomal dominant retinitis pigmentosa:
A;Reference number: A36235; MUID:91051574
A;Accession: A36235
A;Accession: A36235
A;Molecule type: DNA
A;Residues: 18-27 <FAR>
A;Residues: 18-27 <FAR>
                                                                                                                                                                                                                                                                                                       R:Nathans, J.; Hogness, D.S.

Proc. Natl. Acad. Sci. U.S.A. 81, 4851-4855, 1984
A;Title: Isolation and nucleotide sequence of the
A;Reference number: A41200; MUID:84272729
                                                                                                                                                                                                                                                                                                                                                                     C:Species: Homo sapiens (man)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
C:Accession: A41200; A36335; A36537; I51864; I64813; I64814
                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-348 <NAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
OOHU
                                                                                                                                                                                                               A;Cross-references: GB:K02281; NID:g1236136; PIDN:AAC31763 1; R;Farrar, G.J.; Kenna, P.; Redmond, R.; McWilliam, P.; Bradle;
                                                                                                                                                                                                                                                                                             A; Accession: A41200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                 rhodopsin -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A:Genome: mitochondrion
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 2
C:Keywords: membrane-associated complex; mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 KVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 FFQSIMKEKSILEIPTDLLLGLVFISTAFFFKLSAAPFHMWSPDVYEGTLTSIITLFIIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 TKITIFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36 ----IKHRKM--APLDLLLSCLAVSRIF------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 LESHLIIYFLLAVIQ------FLLGIFTNGIIV------VVNGIDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YVPMDKSK----AFVLSFSVLLLTFFCLNPNLII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFNHQ-----IRYISEFTILSKTHP--IIAFSILIILESI------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NATIOKEDTLAIQIFSFVAEFSV-----PLLIFLFAVLLLIFSLGRHTROMRNTVAGSRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKLVPWMILGSLLYVS--MICVFHSKYAGF-----MVPYF------LRKFFSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFI--WLKMRI 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P----PIAGFETKLIVFLTCLKSSLYSLVIFAITISCLATFYYIRIIKIIYFDNCNVWLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGRGAPI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TKFKRFLAYSSINHVGFTMIAVSSINYNGFYSLIFYMMIYILINLGIFASLLSLRNFRNY 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LEMLNLIFYVLATIRRTSEFSTEAGLKYFILGVFSTGLLLFGIALIYGCIGITNFIDLSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A58930; MUID:99030526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------SALLSILSFL------ILYFSHC---MI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.2%;
               the rhodopsin
                                                    R.; Lester, D.H.;
0, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LFINLFGTSLFELFNVWQKLTLICAFFSLFLGTFIAFAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID: 94115781; PIDN: BAA36522.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 124; DB 2;
Pred. No. 0.0054;
9; Mismatches 9
                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      277
                                                                  Jay,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490
                                 in
                                                                                                                                                                                                                                                                                                                            the gene encoding
                                 а
                                                                                                                                                             absence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2
                                                                  3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93;
                               family with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                  Bird,
                                                                                                                                                                                                                 Bradley,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----LQLFIFY
                                                                  A.C.;
                                                                                                                                                           the
                                                                                                                                                                                                               PID:g1236137
Y, D.G.; Hump
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oxidative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID: 94115784
                             autosomal dominant re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164;
                                                                                                                                                                                                                                                                                                                          human rhodopsin.
                                                                                                                                                                                                                                                                                                                                                                                                  21-Jul-2000
                                                                                                                                                       rhodopsin proline->h
                                                                Bhattacharya,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SGI 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                               Humphries,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      phosphorylatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                S
                                                                                                                                                                                                               З
З
```

```
R;Sheffield, V.C.; Fishman, G.A.; Beck, J.S.; Kimura, A.E.; Stone, E.M. Am. J. Hum. Genet. 49, 699-706, 1991
A;Title: Identification of novel rhodopsin mutations associated with retinitis pigmentos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 248-263 <ING>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:120347; OMIM:180380
A;Map position: 3q21.3-3q24
A;Introns: 121/1; 177/2; 232/3; 312/3
A;Note: defects in this gene can result in retinitis pigmentosa C;Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 264-266,'L',268-270 <SH3>
A;Cross-references: GB:S55874; NID:g235662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 14-16,'M',18-20 <SI
A;Cross references: GB:S55797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: I51864; MUID:91377732
A; Accession: I51864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: I64814
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 179-181, 'S',183-185 <SH2>
A; Cross-references: GB:S55799; NID:g235660; PIDN:AAB19831.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I64813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: RHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;62-73/Domain: intracellular #status predicted <IN1>F;74-99/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;1-36/Domain: extracellular #status predicted <EX1>
                                            Ş
                                                                                        밁
                                                                                                                       8
                                                                                                                                                               ₽
                                                                                                                                                                                                  24
                                                                                                                                                                                                                                              밁
. 문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;285-309/Domain: transmembrane #status predicted <TM7>;310-348/Domain: intracellular #status predicted <TM7>;1/Modified site: acetylated amino end (Met) #status predicted ;1/Modified site: acetylated amino end (covalent) #status predicted ;210-187/Disulfide bonds: #status predicted ;210-187/Disulfide bonds: #status predicted ;296/Binding site: retinal (Lys) (covalent) #status predicted ;322,323/Binding site: panintate (Cys) (covalent) #status predicted ;323,323/Binding site: phosphate (Ser) (covalent) (by rhodopsin ;334,338,343/Binding site: phosphate (Thr) (covalent) (by rhodopsin kinase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37-61/Domain: transmembrane #status predicted; 62-73/Domain: intracellular #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :Keywords: acetylated amino end; chromoprotein; eye;
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77-284/Domain: extracellular #status predicted
      188 GIDYYTLKPEVNNE---SFVIYMFVVHFTIPMIIIFFCYGQLVFTVKEAAAQQQES-ATT
                                                                                        148
                                                                                                                                 112
                                                  158
                                                                                                                                                                     88
                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                39
                                              --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS 215
                                                                                                                                                                   LGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR 147
                                                                                                                                                                                                         LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                              MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                                                       ----HPL----FIW----LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                        FGENHAIMGVAFTWVMALACAAPPLAGW:
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                 8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <SHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NID:g235658; PIDN:AAB19830.1; PID:g235659
                                                                                                                                                                                                                                                                                                                              ; Score 123.5; DB 1; ; Pred. No. 0.0044; 63; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s predicted <EX4>
s predicted <TM7>
s predicted <IN4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIDN: AAB19832.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <TM1>
                                                                                                ---SRY----IPEGLQCSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein-coupled receptor; glycol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID:g235663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PID: g235661
                                                                                                                                                                                                                                                                                                                                                                            348;
                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       #status predicte
                                                                                                                                      157
                                                                                                  187
                    243
                                                                                                                                                                                                                                                                                                                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                                         predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΩĄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뮹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
```

```
pheromone receptor VN4 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Natus norvegicus (Provision 02-Aug-1996 #text_change 29-Sep-1999
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 29-Sep-1999
C;Accession: 161746
R;Dulac, C.; Axel, R.
Cell 83, 195-206, 1995
Cell 83, 195-206, 1995
A;Reference number: A57223; MUID:96028094
A;Reference number: A57223; MUID:96028094
A;Accession: 161746
A;Accession: 161746
A;Kotatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-335 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
161746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U36896; NID:g1055249; PIDN:AAC52285.1; PID:g1055250 C;Superfamily: pheromone receptor VN3t
                                                                                                                                                                                                                                 G protein-coupled receptor 41 - human
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1997 #sequence_revision 03-Dec-1997
C;Accession: JC5715
                                                                                      R;Sawzdargo, M.; George, S.R.; Nguyen, T.; Xu, Biochem. Biophys. Res. Commun. 239, 543-547, 15 A;Title: A cluster of four novel human G protei A;Reference number: JC5714, MUID:98008875 A;Accession: JC5715 A;Status: nucleic acid sequence not shown
                                           A; Molecule type: mRNA
A; Residues: 1-346 <SAW>
  A;Cross-references: GB:AF024688; C;Superfamily: G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 63; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 -NPVIYIMMNKQF----RNCMLTTICC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 VREAFFIGLMALSSGYLVAFLWRHRKQAQHLHSTGLSSKSSPEQRATETILLLMSFFVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107
                                                                                                                                                                                                                                                                                                                                                                                                                                       329 CAR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 YILENV--VFYSRMKFKDGSTFYCVQIIVSHSYATVSSFVFIFTEKRMTK-----ILRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 VGILANSILFFGHLCMLLGENKPKPIHLYIASLSLTQLML-LITMGLIAADMFISQGIWD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19 LGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIVIFFIEFIMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QKAEKEVTRMVI IMVIAFLICWVPYASVAFY I FTHQGSNFGPI FMTIPAFFAKSAAIY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L---LLCVLYMCFSSHLI---LSIIATPNLTSDNFMYVTKSCSFLPMCYSRTSMFSTTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYVSMICVFHSKYAGFMVPYFLRKFFSQNAT-----IQKEDTLAIQIFSFVAEFSVPLL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STSCQSLIYLHRLSRGFTLSAACLLNVFWMITLSSKKSCL----TKFKHNSPHHISGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SANCAILLFINELE----LWLATWLGVFYCAKVASVRHPLFIWLKMRISKLVPWMILGSL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YFSHCMIKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILILGNPKLKQNAKKFLLHSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            I---FLFAVL----LLIFSLGRHTROMRNT----VAGSRVPGRGAPISALLSILSFLIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
GB:AF024688; NID:92612947; PIDN:AAB86711.1; PID:92612948 otein-coupled receptor 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 122.5; DB 2; Pred. No. 0.0051;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                putative pheromone receptors in mammals
                                                                                                                                                                          protein-coupled receptor
                                                                                                                                                                                                   ı, S.; Kolakowski Jr., L.F.; O'Dowd,
1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135;
                                                                                                                                                                                                                                                                        #text_change 29-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                               genes occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11;
                                                                                                                                                                                                                                    8
```

```
'B
                                                   õ
                                                                                                8
                                                                                                                                   õ
                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: Z20332

A;Accession: T27253

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-547 <WIL>
A;Cross references: EMBL:AL021501; PIDN:CAA16414.1; GSPDB:GN00023; CESP:Y61B8A.1

A;Experimental source: clone Y61B8A

C;Gene: LCESP:Y61B8A.1

A;Map position: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Y6188A.1 - Caenorhabditis elegans C;Specles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T27253 R;Wall, M. submitted to the EMBL Data Library, January 1998 A;Reference number: Z20332
                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
T27253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: glycoprotein; lipoprotein; thiolester bond F; 18-41/Domain: transmembrane #status predicted <TM1> F; 22-73/Domain: transmembrane #status predicted <TM2> F; 90-111/Domain: transmembrane #status predicted <TM3> F; 132-153/Domain: transmembrane #status predicted <TM4> F; 188-212/Domain: transmembrane #status predicted <TM5> F; 129-250/Domain: transmembrane #status predicted <TM5> F; 229-250/Domain: transmembrane #status predicted <TM6> F; 259-278/Domain: transmembrane #status predicted <TM6- F; 259-278/Domain: transmembrane #status predicted <TM7- F; 166/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                   A; Map position: 5
A; Introns: 121/1; 197/2; 330/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Š
                                                                                                                                                                                                                                                                    Ouery Match 8.1%; Score 122.5; DB Best Local Similarity 24.1%; Pred. No. 0.0077; Matches 66; Conservative 38; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
    379
                                                                                                                                                                                         276
                                                                                                325
                                                                                                                              94 WL-----ATWLGVFYCAKVASVRHPLFIWLKMRISKLVPWMILGSLLYVS-MICVFHSK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 VAGILAATILNELVCEGPYNVSHVVGYICGESPAWRIYVTLLSTLNSCVDDEVYYE 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 ISALL--SILSFLILY----FSH-----C-----MIKVFLSSLKFHIRRFIFLF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171 TLAI----QIFSFVAEFSVPLLIFLFAVLLLIFSLGR---HTROMRNTVAGSRVPGRGAP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 QAGLVSVACWLLASAHCSVVYVIEFSGDISHSQ------GTNGTCYLEFRKD
                                                                                                                                                                                                                                    35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 FLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
LIPEDQDAARQFALTLHPCPTREFFTSEVLIILADNILIERFIWIFPIFGVYFASFPLFQ
                                                                                                                                                                           LINHLECALLDLLLCIESTVYYFLPMYGVEFVGVFSWEGIPNVL----QILL-----V 324
                                                                                                                                                                                                            LIKHRKMAPLDLLLSCLAVSRIFLQLF-IFYVNVIVIFFIEFIMCSANCAILLFINELEL
                                                                                                WLMMMLTGASYVYFFKC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---ISKLVPWMILG---SLLYVSMIC--VFHSKYAGFMVPYFLRKFFSQNATIQ---KED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLAILLPVRLEMAVVLFVVPLIITSYCYSRLVWILGRGGSHRRQRR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANGMHWPLPFILCPLSG--FIFFTTIYL-TALFLAAVSIERFLSVAHPL--WYKTRPRLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                       ----YAGEMVPYFLRKFESQNATIQKEDTLAIQIFSFVAE-FSVPLLIF-LFA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.1%;
                                                                                      --RSSILVQNKFRITRQKTRMIYYSLFFIPWMLTTYFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 122.5; DB 2; Length 346;
Pred. No. 0.0052;
33; M1smatches 93; Indels 79
                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                 547;
                                                                                                                                                                                                                                                                    87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79;
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
  438
                                                                                      378
                                                                                                                                                                                                                        93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             176
                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18;
```

```
C; Superfamily: vertebrate rhodopsin
C; Keywords: chromoprotein; eye; G protein-coupled receptor; glycoprotein; lipoprotein
F; 37-61/Domain: transmembrane #status predicted <TMM2>
F; 14-96/Domain: transmembrane #status predicted <TMM3>
F; 114-133/Domain: transmembrane #status predicted <TMM3>
F; 115-175/Domain: transmembrane #status predicted <TMM4>
F; 203-230/Domain: transmembrane #status predicted <TMM5>
F; 203-276/Domain: transmembrane #status predicted <TMM5>
F; 253-276/Domain: transmembrane #status predicted <TMM5>
F; 255-309/Domain: transmembrane #status predicted <TMM7>
F; 285-309/Domain: transmembrane #status predicted <TMM7>
F; 286/Binding site: retinal (Lys) (covalent) #status predicted
                                                     Š
                                                                                                                                                         Q
                                                                                                           В
                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           opsin - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A23665; S01656
R;Al-Ubaidi, M.R.; Pittler, S.J.; Champagne, M.S.; Triantafyllos, J.T.; McGinnis, J.F.
J. Biol. Chem. 265, 20563-20569, 1990
A;Title: Mouse opsin. Gene structure and molecular basis of multiple transcripts.
A;Reference number: A23665; MUID:91056108
A;Accession: A23665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross-references: GB:M55171; NID:g200144; PIDN:AAA63392.1; PID:g200145 R:Baehr, W.; Falk, J.D.; Bugra, K.; Triantafyllos, J.T.; McGinnis, J.F. FEBS Lett. 238, 253-256, 1988 A:Title: Isolation and analysis of the mouse opsin gene. A:Reference number: S01656; MUID:89005694 A:Accession: S01656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 121/1; 177/2; 232/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: M36695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-348 <BAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-348 <ALA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
     307
                                                   278 ILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                 222
                                                                                                                                                                                                      200 NESFV-----IYMFVVHFTIPMIVIFFCYGQLVFTVKEAAAQQQES-ATTQKAEKE
                                                                                                                                                                                                                                                                       162
                                                                                                                                                                                                                                                                                                               148 FGENHAIMGVVFTWI-MALACAAP-PLVGWSRYIPEGMQCSCGIDY-----YTLKPEVN
                                                                                                                                                                                                                                                                                                                                                                  112 ----HPL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGEMVPYFLRKFFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 FLFCILFQI-----FIPLIAVLPAGWVFIVYL 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 MLAAYM---FILIVIGFPINFITTYYTV------QHKKLRTPLNYILLNLAVADLEMV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 VLLLIF-----SLGRHTROMRNTVAGSRVPGRGAPISALLSILSFLILYFSHCMIKV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                                                                                                                                                                                            QNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRG
IM----LNKQFRNCMLTTLCC
                                                                                             VTRMVIIMVIFFLICWLPYASVAFYIFTHQGSNEGPIFMTLPAFFAKSSSIY---NPVIY 306
                                                                                                                                          APISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLIL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                        FGGFTTTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLSSLKFHIRRFIFLFFILVIGIYPSGHSLILIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSTLIYYICIAPSNTISKDTQQRQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 8.0%; Score 121.5; DB 1 Similarity 20.9%; Pred. No. 0.0063; 67; Conservative 65; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                               221
                                                                                                                                                                                                                                                                                                                                                                     161
                                                                                                                                                                                                                                                                                                                                                                                                                        147
                                                                                                                                                                                                         249
                                                                                                                                                                                                                                                                                                                  199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
```

```
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type; DNA
A;Residues: 1-355 <KAW>
A;Residues: 1-355 <KAW>
A;Cross-references: GB:S79167; NID:g1042072; PIDN:AAB35062.1; PID:g1042073
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Mol. Evol. 40, 594-600, 1995
A;Title: Paralogous origin of the rhodopsinlike opsin genes
A;Reference number: I51319; MUID:95371134
A;Accession: I51319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Anolis carolinensis (green anole)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Aug-1999
C;Accession: I51319
R;Kawamura, S:; Yokoyama, S.;
R;Kawamura, S:; Yokoyama, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: rh2Ac
A;Introns: 121/1; 177/2; 232/3; 312/3
A;Introns: 121/1; 177/2; 232/3; 312/3
C;Superfamily: vertebrate rhodopsin
C;Keywords: chromoprotein; eye; G protein-coupled receptor; lipoprotein; phosphoprotein
C;Keywords: chromoprotein; eye; G protein-coupled receptor; lipoprotein; phosphoprotein
F;296/Binding site: retinal (Lys) (covalent) #status predicted
F;322,323/Binding site: palmitate (Cys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RH2 opsin - green anole
                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
A;Cross-references: GB:AE001179; GB:AE000783; NID:g2688738; PIDN:AAC67146.1; PID:g26887 A;Experimental source: strain B31 C;Superfamily: mviN protein E;1-28/Domain: signal sequence #status predicted <SIG> F;29-512/Product: virulence factor mviN protein homolog #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                      A; Molecule type: DNA
A; Residues: 1-512 <KLE>
                                                                                                                                                               A; Status: preliminary; nucleic acid sequence not shown; translation
                                                                                                                                                                                   A; Reference number: A70100; MUID:98065943
A; Accession: A70201
                                                                                                                                                                                                                                 Nature 390, 580-586, 1997
A;Authors: Smith, H.O.; Venter, J.C.
A;Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 8.0%;
Best Local Similarity 23.6%;
Matches 62; Conservative 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFSQNATIQK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIVIFFIEFIMCSANCAILLFI----NELELW-----LATWLGVFYCAKVASVR----HPL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYFLLAVIQELLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQLFIFYVN 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESYV---LYMFGVHFVIPVVVIFFSYGRLICKVREAAAQQQES-ASTQKAEREVTRMVIL 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGISFTWF-MSFSCAAP-PLLGWSRYIPEGMQCSCGPDY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FYTAWNGYFIFGPIGCAIEGFFATLGGQVALWSLVVLAIERYIVVCKPMGNFRFSATHAL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MVLGELLAWTPYAMVAFWIFTNK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SILSFLILYFSHCMIKVFLSSLK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGSRVPGRGAPISALL 228

    k; Score 121; DB 2; Length 355;
    k; Pred. No. 0.0071;
    43; Mismatches 112; Indels

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----YTLNPDYHN 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46;
                                                                                                                                                                           not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                                      White
Vugt,
B.
```

```
Š
                                                                                                                                                                                                                                                 ₽
                          γQ
                                                           밁
                                                                                        Qy
                                                                                                                         밁
                                                                                                                                                    δÃ
                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                               QΥ
밁
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                  136 YLVLYILLISLSSI-----FVSVLNSYKIFFIPSFSPIMLSFG-----IILSIFLFY 182
                                                                                             160
                                                                                                                           228
                                                               281
                                                                                                                                                                                                                                                                                5 HLIIYELLAVIQELLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLEIFY 64
                             VAGSRVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHI 254
                                                               YISIATV-----
                                                                                         FSQNATIQKEDTLAIQIFSFVAEFSV-----PLLIFLFAVLLLIFSLGRHTROMRNT 211
                                                                                                                         LNFLTRWLRMIFGFSISIITQQIS-----FALASTLEIGSVSILSNAVVYYQLPVGI--F
                                                                                                                                                     I-----WLKM------RISKLVPWMTLGSLLYVSMICVFHSKYAGFMVPYFLRKF 159
                                                                                                                                                                                      GREGIYSAVIGVIFGGELQFLIPFANCLMIGF-----AWKPTFY-----FREKVF
                                                                                                                                                                                                                    ------VNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLF 115
   ----IP-----
                                                                                                                                                                                                                                                                                                                     60;
                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                  8.0%; Score 121; DB 1; Length 512; 21.2%; Pred. No. 0.0097;
 ----VSFLMFIWSDYILNLFLMGGKFSI 345
                                                               IFPKMAEHAVLGNNIKLNALLVDGIKILLLIF---
                                                                                                                                                                                                                                                                                                                   43;
                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                          74;
                                                                                                                                                                                                                                                                                                                          Indels 106;
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                         319
                                                                                                                                     280
                                                                                                                                                                                                                                                                                                                             13;
```

Search completed: March 15, 2001, 13:00:06 Job time: 467 sec

98.50

98

98.50 159.

165.36 0 0

0.1170

```
/cgn2_6/ptcdata/2/lna/5A_COMB.seq:US-08-031-99-4
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-931-99-4
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-931-99-4
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-820-931-1
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-6103a-1
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-6103a-1
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-646-103a-1
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-646-103a-1
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-646-93-1
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-644-93-106.00
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-644-93-106.00
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-644-93-106.00
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-644-93-106.00
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-647-931-7
/cgn2_6/ptcdata/2/lna/5B_COMB.seq:US-08-139-175-7-104-50-175-59-0.0315-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-88-13-195-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM of: US-09-510-332-1 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database: Issued_Patents_NA:*
Database sequences: 280836
Database length: 80580151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search information blo
Query: US-09-510-332-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MODEL=frame+_D2n.model -DEV=xlp
-MODEL=frame+_D2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool/US09510332/runat_06032001_093637_13647/app_query.fasta_1.359
-Q=/cgn2_1/USPTO_spool/US09510332/runat_06032001_093637_13647/app_query.fasta_1.359
-DB=ISSued_patents_NA -QFMT=fastap -SUFFIX=rni -GAPOP=12.000
-GAPOEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOEXT=0.000 -XGAPOP=10.000 -XGAPOEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPOEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -START=1 -MATRIX=blosum62
-DELOY=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=PCt
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=PCt
-TRANS=human40.cdi -LIST=45 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -MAXLEN=200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-805-123C-1 + /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-033-081B-1 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        score_list:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -USER-US09510332_@CGN1_1_54 -NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strd Orig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      out_format : pfs
98.50
98.50
98.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210.63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0.0004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1080 !
0.0217
7600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.0433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.3324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1958
19124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1960 !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1872
1872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-06380-3 + /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-966-316-6 + 96 /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-982-493-7 + 98 /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-468-036-38 - /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-376-843-38 - /cgn2_6/ptodata/2/ina/5B_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-805-123C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1,
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Appi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3016
```

```
seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-805-123C-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                               alignment_block:
US-09-510-332-1 x US-07-805-123C-1
                                                                                                                                                                                                         Align seg 1/1 to: US-07-805-123C-1 from: 1
                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dryja, Thaddeus
APPLICANT: Berson, Eliot L.
TITLE OF INVENTION: DIAGNOS
TITLE OF INVENTION: DEGENER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PS/2 Model 50Z or 55S;
OPERATING SYSTEM: MS-DOS (Version 5
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 07/469,215
FILING DATE: January 24, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Clark Paul T.
REGISTRATION NUMBER: 30,162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1991121
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                                                                                                              409 ATGCTGGCCGCCTACATG.....TTTCTGCTGATCGTGCTGGGCTT 449
                                                          450 CCCCATCAACTTCCTCACGCTCTACGTCACCGTC....
34 spLeuIleLysHisArgLysMet...AlaProLeuAspLeuLeuLeuSer 49
                                                                                          17 eLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US
FILING DATE: 19911211
                                                                                                                                                                   1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dryja, Thaddeus P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ication US/07805123C
                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                        124.50
0.759
50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DIAGNOSIS OF HEREDITARY RETINAL DEGENERATIVE DISEASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/07/805,123C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>..</u>
                                                                                                                                                                                                                                                                                                            Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00246/069003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.0)
                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                 to: 3016
                                                                                                                                                                                                                                                                                                            328
16
20.732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.50 156.92 0.3454
98.50 156.92 0.3454
                                                                    483
```

seq_documentation_block: seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-033-081B-1

<pre>iCACAAGAAGCTGCGCACGCCTCTCA ilSerArgIlePheLeuGlnLeuPhe ::: ::: CGCTGACCTCTTCATGGTCCTAGGT</pre>	1 MetleuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17	Align seg 1/1 to: US-08-033-081B-1 from: 1 to: 3016	alignment_block: US-09-510-332-1 x US-08-033-081B-1	alignment_scores: Ouality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.732	ONESS: dou 7: linear -1	ORMATION FOR SEQ ID NO: EQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid	TELEFAX: (617) 542-8906 TELEX: 200154	EFERENCE/DOCKET NUMBER: 0 ECOMMUNICATION INFORMATION ELEPHONE: (617) 543-5070	INFORMATION: , Paul T. NUMBER: 30,16	OF INVENTION: DEGENERATIVE OF INVENTION: DEGENERATIVE	PLICANT: Dryja, The	C NO. 54
	eLeuLeuGlyIlePheThrAsnGlyIleIl	MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17	ign seg 1/1 to: US-08-033-081B-1 from: 1 to: 3016 1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17	lignment_block: US-09-510-332-1 x US-08-033-081B-1 Align seg 1/1 to: US-08-033-081B-1 from: 1 to: 3016 1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlavalIleGlnPh 17	lignment_scores: Quality: 124.50 Ratio: 0.759 Retio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.732 lignment_block: US-08-033-081B-1 Align seg 1/1 to: US-08-033-081B-1 I MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17	STRANDEDNESS: double TOPOLOGY: linear 1.lignment_scores:	INCOMMATION OF THE SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1	TELEFAX: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_scores: Ouality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.732 lignment_block: US-08-033-081B-1 I MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17	REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-8906 TELEX: 200154 TELEPAX: (617) 542-8906 TELEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_scores: Quality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Similarity: 50.000 Percent Similarity: 50.000 Ratio: 0.759 Percent Similarity: 50.000 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.732 Lignment_block: US-08-033-081B-1 IMELLEUGIUSETHISLEUTIELITYTPHELEULEUALAVAILLEGInPh 17	NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: TISH & RICHARDSON STREET: 225 Franklin Street CITY: Boston STATE: MASSACHUSELTS COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER RENDABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER RENDABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.54 Mb COMPUTER: LBM PS/2 Model 50Z or 55SX OPERATICS STEEM: MS-OOS (Version 5.0) SOFTWARE: Wardberfect (Version 5.1) APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1933 CLASSIFICATION DATA: APPLICATION NUMBER: 07/845,226 FILING DATE: January 23, 1990 APPLICATION NUMBER: 07/845,226 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/845,226	TITLE OF INVENTION: DIAGNOSIS OF HEREDITARY RETINAL TITLE OF INVENTION: DEGENERATIVE DISEASES NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STREET: 225 Franklin Street CITY: Boston COMPUTER EADABLE FORM: COMPUTER STEM: MS-DOS (Version 5.0) SOFTWARE: HOW BORTON OPERATING SYSTEM: WS-DOS (VERSION 5.1) CURENT APPLICATION NUMBER: U5/08/033,081B FILING DATE: JANUARY 23, 1992 APPLICATION NUMBER: 07/825,296 FILING DATE: JANUARY 24, 1990 APPLICATION NUMBER: 07/825,296 APPLICATION NUMBER: 07/825,296 FILING DATE: JANUARY 24, 1990 APPLICATION NUMBER: 07/825,296 APPLICATION NUMBER: 07/825	APPLICANT: Dryla, Thaddeus P. APPLICANT: Dryla, Thaddeus P. APPLICANT: Brison, Ellot L. TITLE OF INVENTION: DISCASSIS OF HEREDITARY RETINAL TITLE OF INVENTION: DEGENERATIVE DISEASES NUMBER OF SEQUENCES: 25 NOTERATION MASSACHUSETLS COUNTRY: U.S.A. ZIP: O2110-2260 COMPUTER: HASSACHUSETLS COUNTRY: U.S.A. ZIP: O2110-2260 COMPUTER: HASSACHUSETLS COUNTRY: U.S.A. ZIP: D2110-1260 COMPUTER: HASSACHUSETLS COUNTRY: U.S.A. ZIP: D2110-1260 COMPUTER: HASSACHUSETLS COUNTRY: U.S.A. ZIP: D2110-1260 MEDIUM TYPE: 3.5" DISKETLE, 1.44 Mb COMPUTER: HASSACHUSETLS COMPUTER: H
spLeuIleLysHisArgLysMetAlaProLeuAspLeuLeuSer 49 ::: ::: ::: ::: ::: :::		1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17	ign seg 1/1 to: US-08-033-081B-1 from: 1 to: 3016 1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaVallIleGlnPh 17	lignment_block: US-09-510-332-1 x US-08-033-081B-1 Align seg 1/1 to: US-08-033-081B-1 from: 1 to: 3016 1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaVallleGlnPh 17	lignment_scores: Quality: 124.50 Quality: 0.759 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.732 lignment_block: US-08-033-081B-1 Align seg 1/1 to: US-08-033-081B-1 I MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17	STRANDEDNESS: double TOPOLOGY: linear 15-08-033-081B-1 Length: 328 Quality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Similarity: 50.000 Percent Identity: 20.732 lignment_block: US-08-033-081B-1 US-09-510-332-1 x US-08-033-081B-1 Align seg 1/1 to: US-08-033-081B-1 I MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh H -	SEQUENCE CHARACTERISTICS: LENGTH: 3016 LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Length: 328 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.732 lignment_block: US-08-033-081B-1 lignment_block: US-08-033-081B-1 Align seg 1/1 to: US-08-033-081B-1 I MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17	TELEFAX: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-03-081B-1 Lignment_scores: Oublity: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.732 lignment_block: US-08-033-081B-1 lignment_block: US-08-033-081B-1 lignment_block: US-08-033-081B-1 Align seg 1/1 to: US-08-033-081B-1 IMELEUGIUSERHISLEUIIEIIETyrPheLeuLeuAlaValIleGlnPh IMELEUGIUSERHISLEUIIETYRPHELEULEUALaValIleGlnPh IMELEUGIUSERHISLEUIIETYRPHELEULEUALaValIleGlnPh IMELEUGIUSERHISLEUIIETYRPHELEULEUALaValIleGlnPh IMELEUGIUSERHISLEUIIETYRPHELEULEUALAVAIIIEGUIPH IMELEUGIUSERHISLEUIIETYRPHELEULEUALAVAIIIEGUIPH IMELEUGIUSERHISLEUIIETYRPHELEULEUALAVAIIIEGUIPH IMELEUGIUSERHISLEUIIETYRPHELEULEUALAVAIIIEGUIPH IMELEUGIUSERHISLEUIIETYRPHELEULEUALAVAIIIEGUIPH IMELEUGIUSERHISLEUIIIETYRPHELEULEUALAVAIIIEGUIPH IMELEUGIUSERHISLEUIIIETYRPHELEULEUALAVAIIIEGUIPH IMELEUGIUSERHISLEUIIIETYRPHELEULEUALAVAIIIEGUIPH IMELEUGIUSERHISLEUIIIETYRPHELEULEUALAVAIIIEGUIPH IMELEUGIUSERHISLEUIIIETYRPHELEUULEUALAVAIIIEGUIPH IMELEUGIUSERHISLEUIIIETYRPHELEUULEUALAVAIIIIEGUIPH IMELEUGIUSERHISLEUIIIETYRPHELEUULEUALAVAIIIIEGUIPH IMELEUGIUSERHISLEUULEUALAVAIIIIEGUIPH IMELEUGIUSERHISLEUULEUALAVAIIIIEGUIPH IMELEUGIUSERHISLUU	REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-8906 TELEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear IS-08-033-081B-1 Iignment_scores: Quality: 124.50 Ratio: 0.759 Ratio: 0.759 Percent Similarity: 50.000 Percent Similarity: 50.000 Ratio: 0.759 Iignment_block: US-08-033-081B-1 I MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17 IIIII IIII IIIII IIIIII IIIIIIII	NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: rish 4 Richardson STREET: 225 Franklin Street CITY: Boston STREET: 202110-2804 COMPUTER: LDA STREET: MS-DOS (Version 5.0) SOFTWARE: STREET: MS-DOS (Version 5.0) SOFTWARE: Washolder (version 5.1) COMPUTER: LDA STREET: US/08/033/081B FILING DATE: MS-DOS (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: 05/08/033/081B FILING DATE: January 23, 1992 FILING DATE: January 23, 1992 FILING DATE: January 24, 1990 AFFORMATION NUMBER: 00,162 FILING DATE: January 24, 1990 AFFORMATION NUMBER: 30,162 FILING DATE: January 24, 1990 AFFORMATION INFORMATION: REFERENCE/DOCKET NUMBER: 00246/069005 FILING DATE: January 24, 1990 AFFORMATION FOR SEQ ID NO: 1: REGISTRATION SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: TELEPHONE: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: TYPE: DICLEIC acid STRANDEDNESS: double TYPE: DICLEIC acid STRANDEDNESS: John Seq ID NO: 1: SEQUENCE CHARACTERISTICS: TYPE: DICLEIC acid STRANDEDNESS: John Seq ID NO: 1: SEQUENCE CHARACTERISTICS: Length: 328 FILING JOHN SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: DESCRIPTION: JOHN SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: Length: 328 SEQUENCE CHARACTERISTI	TITLE OF INVENTION: DIAGNOSIS OF HEREDITARY RETINAL TITLE OF INVENTION: DEGENERATIVE DISEASES NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STREET: 325 Franklin Street COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER: IN #8272 Model 502 or 555x OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTMARE: MOTOPER FORM: MEDIUM TYPE: 3.5" DISkette, 1.44 Mb COMPUTER: IN #82/2 Model 502 or 555x OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTMARE: MOTOPER FORM: MEDIUM TYPE: 0.5" MS-DOS (Version 5.0) SOFTMARE: MOTOPER FORM: MEDIUM TYPE: 0.5" MS-DOS (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: 02/08/033.081B FILING DATE: MATCH 11, 193 CLASSIFICATION NUMBER: 07/852,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/852,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 APPLICATION NUMBER: 07/469,215 APPLICATION NUMBER: 07/469,215 APPLICATION NUMBER: 00/469,025 FILING DATE: January 23, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REFERENCE/DOCKET NUMBER: 00246/069005 TELEFAX: (617) \$42-8906 INFORMATION FOR SEQ ID NO: 1: RESIDENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DUCLELC acid STRANDENNESS: double TYPE: DUCLEC CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: LENGTH: 3016 STRANDENNESS: double TYPE: DUCLEC CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3026 FILE GAPS: 11 near 1.14nnant: 100-100 1.14nnant: 100-100 1.15nnant: 100-100	APPLICANT: Dryla, Thaddeus P. APPLICANT: Dryla, Thaddeus P. APPLICANT: Berson, Eliot L. TITLE OF INVENTION: DIGENERATIVE DISEASES NUMBER OF SEQUENCES: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS; ADDRESSE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STREET: 225 Franklin Street CITY: Boston STREET: 225 Franklin Street COUNTRY: U.S.A. ZIP: 02101-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" DISKette, 1.44 kb COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" DISKette, 1.44 kb COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" DISKette, 1.44 kb COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" DISKette, 1.44 kb COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" DISKette, 1.44 kb COMPUTER READABLE FORM: MEDIUM TYPE: JS" MODEL 50 or 555X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: HANDER: WS-DOS (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: U.7080,33,081B FILING DATE: January 23, 1992 APPLICATION NUMBER: 07,7455,296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07,745,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 00246/069005 FILECOMMUNICATION INFORMATION: NAME: Clark, Paul T. APPLICATION NUMBER: 00246/069005 TELEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 STRANDEDNESS: double TOPOLOGY: linear 11squament_scores: 11squament_scores: 11squament_scores: 11squament_block: US-08-033-081B-1 1409 MCCTGCCCCCTACATG:
NAME: Clark, Paul T. NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_scores: Ouality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Jinearity: 50.000 Ratios: 0.759 Percent Similarity: 50.000 Ratios: 0.759 Percent Similarity: 50.000 Ratio: 0.759 Percent Jinearity: 124.50 Ratio: 0.759 Ratio: 0	NAME: Clark, Paul T. NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 lignment_scores: Quality: 124.50 Quality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Joundary: 0.759 lignment_block: US-08-033-081B-1 Align seg 1/1 to: US-08-033-081B-1 from: 1 to: 301	NAME: Clark, Paul T. NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMBUNICATION: INFORMATION: TELEPHONE: (617) 542-8906 TELEEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: 1inear Is-08-033-081B-1 LIGNMENT_SCORES: Ouality: 124.50 Retio: 0.759 Percent Similarity: 50.000 Percent Jinear Ingnment_block: US-08-033-081B-1 Retio: 0.759 Retio: 0.759 Percent Similarity: 50.000 Retio: 0.759 Re	NAME: Clark, Paul T. NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMBUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 TELEFX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_scores: Ouality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.73	ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 TELEEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear TOPOLOGY: linear	NAME: CLAIR', PAUL T REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 TELEX: 200154 TELEX: 200154 TELEX: 200154 TELEX: 3016 TELEX: 3016 TELEX: 3016 TELEX: 3016 EQUENCE CHARACTERISTICS:	ITTOKNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 REFERENCE/DOCKET NUMBER: 00246/06900 REJECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 TELEFAX: 200154	ITTOKNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 547-577	INFORMATION: , Paul T. NUMBER: 30.16		MBER OF SEQUENCES: 25 ADDRESSED: Fish & Richardson STREET: 225 Franklin Street CITY: Boston 2210-2804 COUNTRY: U.S.A. 20110-2804 MEDIUM TYPE: 3.5" Diskette, 1.4 COMPUTER READABLE FORM: MS-DOS COPERATING SYSTEM MS-DOS (Version PREVIARRE: Wordperfect (Version RRENT ARPLICATION LOATA: APPLICATION: 435 CLASSIFICATION NUMBER: 07/825,296 TILING DATE: March 11, 193 CLASSIFICATION NUMBER: 07/825,296 TOR APPLICATION NUMBER: 07/825,296	TLE OF INVENTION: DIGGNERATIVE DISEASES MBER OF SEQUENCES: 25 MBER OF SEQUENCES: 25 RRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 MPUTER READABLE FORM: MPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 502 or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WorldPerfect (Version 5.1) RRENT APPLICATION DATA: APPLICATION UNMBER: US/08/033,081B FILING DATE: March 11, 193 CLASSIFICATION DATA: IOR APPLICATION DATA: APPLICATION UNMBER: 07/825,296	PLICANT: Dryja, Thaddeus P. PLICANT: Berson, Eliot L. PLICANT: Berson PRESSES: Fish & Richardson PREDIUM TYPE: 3.5" Diskette, 1.44 Mb PREDIUM TYPE: JS-Z PERATING SYSTEM: MS-DOS (Version 5.0) PRESSESSES PRESSES PRE
APPLICATION NUMBER: 07465,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEEAX: (617) 542-8906 INFORMATION POR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear 1.lignment_Scores: Quality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.732 lignment_block: US-08-033-081B-1 1.lignment_block: US-08-033-081B-1 1.lignment_block: US-08-033-081B-1 from: 1 to: 3016 1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17	APPLICATION NUMBER: 074469.215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 1.ignment_scores: Quality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.73 1.ignment_block: US-08-033-081B-1 Lingth: 1 to: US-08-033-081B-1 Align seg 1/1 to: US-08-033-081B-1 from: 1 to: 301	APPLICATION NUMBER: 074469.215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30.162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 lignment_scores:	APPLICATION NUMBER: 074469.215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30.162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear IS-08-033-081B-1 Lignment_scores: Ouality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.73	APELICATION NUMBER: 074469.215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear TOPOLOGY: linear	APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark, Paul T REGISTRATION NUMBER: 00246/06900 REFERENCE/DOCKET NUMBER: 00246/06900 ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-8906 TELEX: 200154 TELEX: 200154 CORMATION FOR SEQ ID NO: 1: EQUENCE CHARACTERISTICS: ELNGTH: 3016 TYPE: nucleic acid	APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEFAX: (617) 542-8906 TELEFAX: 200154	APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 547-577	NUMBER: 07/469,21 January 24, 1990 INFORMATION: , Paul T. , Paul T.	January 24, 1990 January 24, 1990	MBER OF SEQUENCES: 25 ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. COUNTRY: U.S.A. MEDIUM TYPE: 3.5" Diskette, 1.4 MEDIUM TYPE: 3.5" Diskette, 1.4 COMPUTER: IBM PS/2 Model 502 or OPERATING SYSTEM: MS-DOS (Version SOPERATING SYSTEM: MS-DOS (Version RRENT APPLICATION DATA: APPLICATION UMBER: US/08/033,0 FILING DATE: March 11, 1993 CLASSIFICATION: 435	TLE OF INVENTION: DIAGNOSIS OF HEREDITARY TLE OF INVENTION: DEGENERATIVE DISEASES MBER OF SEQUENCES: 25 MBER OF SEQUENCES: 25 FREESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.54 Mb MEDIUM TYPE: 3.5" Diskette, 1.54 Mb MEDIUM TYPE: 3.5" DOSK (Version 5.0) SOFTWARE: WOrdperfect (Version 5.1) RRENT APPLICATION DATA: RRENT APPLICATION DATA: REIN MATCH 11, 1993 CLASSIFICATION: 435 CLASSIFICATION: 435	LICANT: Dryja, Thaddeus P. LICANT: Berson, Ellot L. RICANT: Berson, Ellot L. RICANT: Berson, Ellot L. RICANT: Berson, Ellot L. RICANT: Berson, Ellot L. RESPONSING ADDRESS: ABER OF SEQUENCES: 25 RESPONDENCE ADDRESS: LTY: BOSTON STREET: 225 Franklin Street STATE: Massachusetts COUNTRY: U.S.A. FOUNTRY: U.S.A. FOUNTRY: U.S.A. FOUNTRY: J.S.A. SOUNTRY: J.S.A. FOUNTRY: J.S.A. SOUNTRY: J.S.A. FOUNTRY: J.S.A. FOUNTRY: J.S.A. SOUNTRY: J.S.A. SOUNTRY: J.S.A. FOUNTRY: J.S.A. SOUNTRY: J.S.A. FOUNTRY: J.S.A. SOUNTRY: J.S.A. FOUNTRY: J.S.A. FOUNTRY: J.S.A. FOUNTRY: J.S.A. FOUNTRY: J.S.A. J.S.A. SOUNTRY: J.S.A. J.S.A. SOUNTRY: J.S.A. J.S.A
PRIOR APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 TELEFAX: (617) 542-8906 TELEFAX: (617) 542-8906 TELEFAX: (617) 542-8906 TELEFAX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_block: US-08-033-081B-1 Lignment_block: US-	PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 RELEFAX: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 30246/069005 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 30246/069005 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 30246/069005 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 30246/069005 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 30246/069005 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 30246/069005 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 30246/069005 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 30246/069005 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 30246/069005 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 30246/069005 INFORMA	APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEPAX: (617) 542-8906 TELEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DUCLHEC acid STRANDEDNESS: double TOPOLOGY: linear IS-08-033-081B-1 Lignment_scores:	APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION STRICT acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear Is-08-033-081B-1 Lignment_scores: Ouality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.73	PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,162 REFERENCE,DOCKET NUMBER: 00246/06900 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DUCLE: acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1	APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00.246/06900 REGISTRATION HABER: 00.246/06900 RECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5970 TELEFAX: (617) 542-5970 TELEFAX: 200154 TELEFAX: 200154 ORMATION GOR SEQ ID NO: 1: EQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid	RIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/06900 ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEFAX: 200154	RPICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/06900 ELECOMMUNICATION INFORMATION: TELEPHONE: 6617,567670	ION DATA: NUMBER: 07/825,29 January 23, 1992 NUMBER: 07/469,21 January 24, 1990 INFORMATION: POUL T. POUL T. NUMBER: 30,162	ION DATA: NUMBER: 07/825,29 January 23, 1992 NUMBER: 07/469,21 January 24, 1990	MBER OF SEQUENCES: 25 ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: MSSachusetts COUNTRY: U.S.A. COUNTRY: U.S.A. COUNTRY: U.S.A. COUNTRY: U.S.A. EDIIO 710-2804 MEDIUM TYPE: 3.5" Diskette, 1.4 MEDIUM TYPE: 3.5" Diskette, 1.4 MEDIUM TYPE: 3.5" DOS (Version OPERATING SYSTEM: MS-DOS (Version SOFTWARE: Wordperfect (Version STATE) SOFTWARE: Wordperfect (Version STATE) RENT APPLICATION DATA:	TLE OF INVENTION: DIGGNERATIVE DISEASES MBER OF SEQUENCES: 25 MBER OF SEQUENCES: 25 MBER OF SEQUENCES: 25 MBER OF SEQUENCES: 25 MDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. COUNTRY: U.S.A. ZIP: 02110-2804 MPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READABLE FORM: MEDIUM TYPE: MS-DOS (Version 5.0) OPERATING SYSTEM: MS-DOS (Version 5.1) SOFTWARE: WOrdPerfect (Version 5.1) SOFTWARE: WOrdPerfect (Version 5.1) REENT APPLICATION DATA:	PLICANT: Dryja, Thaddeus P. PLICANT: Berson, Ellot L. PERSONDENCE ADDRESS: PLE OF INVENTION. DECEMERATIVE DISEASES BER OF SEQUENCES: 25 RESPONDENCE ADDRESS: PLANTISE Fish & RIChardson PRESSEE: J. S. Diskette, 1.44 Mb PRESSEE: J
FILING DATE: March 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: 07/825,296 APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELEFAX: (617) 542-5070 TELEFAX: (617) 542-8906 TELEFAX: (617) 542-8906 TELEFAX: 200134 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear Is-08-033-081B-1 Lignment_block: US-09-510-332-1 x US-08-033-081B-1 IMETLEGISTRATION: INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 IMETLEGISTRATION: INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear IS-08-033-081B-1 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 328 Gaps: 316 Gaps: 316 Gaps: 326 Gaps: 327 Gaps: 328 Gaps: 328 Gaps: 328 Gaps: 326 Gaps: 328 Gap	FILING DATE: March 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEX/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEFAX: (617) 542-8906 TELEFAX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: INCLEAR COULDING TOPOLOGY: linear S-08-033-081B-1 lignment_block: US-08-033-081B-1 Length: 32 Percent Similarity: 50.000 Percent Identity: 20.73 lignment_block: US-08-033-081B-1 Align seg 1/1 to: US-08-033-081B-1 from: 1 to: 301	FILING DATE: March 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: 07/825,296 APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/069005 TREEDOMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-8906 TELEEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TYPE: nucleic acid STRANDEDNESS: double TYPE: 002114y: 110ear 11gnment_scores:	FILING DATE: March 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/869,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 RELECANDUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 TELEFX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear STANDEDNESS: linear 11gnment_scores:	FILING DATE: March 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00/246/06900 TELEPHONE: (617) 542-5070 TELECAMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear	FILING DATE: MATCH 11, 1993 CLASSIFICATION: 435 RIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,162 REGISTRATION NUMBER: 00246/06900 ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-8906 TELEX: 200154 ORMATION FOR SEQ ID NO: 1: EQUENCE CHARACTERISTICS: EQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid	FILING DATE: MATCH 11, 1993 CLASSIFICATION: 435 RIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark, Paul T REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 TELEFAX: (617) 542-8906 TELEFAX: (617) 542-8906 TELEEPAX: 200154	FILING DATE: MATCH 11, 1993 CLASSIFICATION: 435 RIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 REFERENCE/DOCKET NUMBER: 00246/06900 REFERENCE/DOCKET NUMBER: 00246/06900	March 11, 1993 ON: 435 ION DATA: ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/469,215 January 24, 1990 INFORMATION: Paul T. Paul T. NUMBER: 30.162	March 11, 1993 ON: 435 ION DATA: ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/469,215 January 24, 1990	P SEQUENCES: 25 NDENCE ADDRESS: SEE: Fish & Richardson : 225 Franklin Street Boston Massachusetts Y: U.S.A. 02110-2804 READABLE FORM: READAB	OF INVENTION: DIAGNOSIS OF HEREDITARY OF INVENTION: DEGENERATIVE DISEASES R OF SEQUENCES: 25 SPONDENCE ADDRESS: SPONDENCE ADDRESS: SPONDENCE ADDRESS: FISH & RICHARDSON EET: 225 Franklin Street Y: Boston FIE: Massachusetts Y: Boston FIE: Massachusetts V: Boston FIE: Massachusetts U.S.A. 102110-2804 FIE: MS-DOS (Version 5.0) FIR READABLE FORM: FORM: MS-DOS (Version 5.0) FIR READABLE FORM: MS-DOS (Version 5.0)	LICANT: Dryja, Thaddeus P. LICANT: Berson, Eliot L. LICANT: DEGENERATIVE DISEASES ABER OF SEQUENCES: 25 ABER OF SEQUENCES: 25 ABER OF SEQUENCES: 25 ADDRESSE: Fish & Richardson STREET: 225 Franklin Street LITY: Boston LITY: DISEACH LITY:
CURENT APPLICATION NUMBER: US/08/033.081B FILLING DATE: MATCH 11, 1993 CLASSIFICATION AUMBER: US/08/033.081B FILLING DATE: MATCH 11, 1993 CLASSIFICATION AUMBER: 07/825,296 FILLING DATE: JANUARY 23, 1992 APPLICATION NUMBER: 07/85,296 FILLING DATE: JANUARY 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/069005 TELEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DUCLEC CHARACTERISTICS: LENGTH: 328 TYPE: DUCLEC CHARACTERISTICS: LENGTH: 329 TYPE: DU	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 RELEFAN: (617) 542-8906 TELEFAN: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear TOPOLOGY: linear S-08-033-081B-1 Lignment_Bock: US-08-033-081B-1 Lignment_block: US-08-033-081B-1 from: 1 to: 301 Align seg 1/1 to: US-08-033-081B-1 from: 1	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/03,081B FILING DATE: MATCH 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION NUMBER: 00246/069005 TELEPHONE: (617) 542-8906 TELEPHONE: (617) 542-8906 TELEPHONE: (617) 542-8906 TELEPHONE: ONCOMENT ON SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear STRANDEDNESS: double TOPOLOGY: linear 11gnment_scores:	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 REFERENCE (617) 542-8906 TELEFAX: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_scores: Ouality: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.73	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: 00246/06900 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8006 TELEEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 STRANDEDNESS: double TOPOLOGY: linear TOPOLOGY: linear S-08-033-081B-1	URRENT APPLICATION DATA: APPLICATION UMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION: 435 RIOR APPLICATION DATA: APPLICATION UMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 RELEPHONE: (617) 542-5970 TELEPHONE: (617) 542-5970 TELEFAX: (617) 542-8906 TELEFAX: 200154 ORMATION FOR SEQ ID NO: 1: EQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid	URRENT APPLICATION DATA: APPLICATION UMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION 435 CLASSIFICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/06900 ELECOMMUNICATION INFORMATION: TELEPAY: (617) 542-8906 TELEFAY: (617) 542-8906 TELEX: 200154	URRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION: 435 CLASSIFICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/06900 REGERENCE/DOCKET NUMBER: 00246/06900 TELEPHONE: (617) 547-5770	ATION DATA: ATION DATA: NUMBER: US/08/033,081B March 11, 1993 ON: 435 ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/469,215 January 24, 1990 INFORMATION: Paul T. Paul T. NUMBER: 30.162	ATION DATA: ATION DATA: NUMBER: US/08/033,081B MATCH 11, 1993 ON: 435 ION DATA: IO	P SEQUENCES: 25 NDENCE ADDRESS: SEE: Fish & Richardson : 225 Franklin Street Boston Massachusetts Y: U.S.A. Y: U.S.A. READABLE FORM: READABLE FORM: READABLE JOISKette, 1.4	OF INVENTION: DIAGNOSIS OF HEREDITARY OF INVENTION: DEGENERATIVE DISEASES OF INVENTION: DEGENERATIVE DISEASES OF INVENTION: DEGENERATIVE DISEASES SPONDENCE ADDRESS: SPONDENCE ADDRESS: FRESSEE: Fish & Richardson EET: 225 Franklin Street Y: Boston Fish Assachusetts Y: Boston Fish Massachusetts VIS.A. INTRY: U.S.A. INTRY: U.S	PLICANT: Dryja, Thaddeus P. PLICANT: Berson, Ellot L. PERSON DERCE ADDRESS: POERSESEE: Fish & Richardson PATE: Plassachusetts POUNTRY: U.S.A. PUTER READABLE FORM: #EDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50% or 555% OPERATING SYSTEM: MS-DOS (VERSION 5.0) SOFTWARE: WORDERFECT (VERSION 5.1) CURRENT APPLICATION DATA: APPLICATION UNWBER: US/08/033,081B FILING DAYE: MARCH 11, 1993 CLASSIFICATION NUMBER: 07/825,296 FILING DAYE: MARCH 11, 1993 CLASSIFICATION NUMBER: 07/825,296 FILING DAYE: January 24, 1990 APPLICATION NUMBER: 07/469,215 FILING DAYE: January 24, 1990 APPLICATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 FELEGAMINICATION INFORMATION: REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 FELEGAM: (617) 542-8906 FELEGAM: (COMPUTER: IBM PS/Z MODEL 50% or 558x OPERATING SYSTEM: MS-DOS (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: MATCH 11, 1993 CLASSIFICATION NUMBER: U7/825,296 FILING DATE: MATCH 11, 1993 APPLICATION NUMBER: 07/825,296 FILING DATE: JANUARY 23, 1992 APPLICATION NUMBER: 07/825,296 FILING DATE: JANUARY 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: NUCLEIC acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Length: 32-1 S-08-033-081B-1 Lignment_block: US-08-033-081B-1 from: 1 to: 301 Align seg 1/1 to: US-08-033-081B-1 from: 1	COMPUTER: IBM PS/Z Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: MATCH 11, 1993 CLASSIFICATION NUMBER: 07/825,296 APPLICATION NUMBER: 07/469,215 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 TELEFONMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear OPOLOGY: linear 11gnment_scores: Ouality: 124.50 Percent Similarity: 50.000 Percent Similarity: 50.000 Percent Similarity: 50.000 Percent Similarity: 50.001	COMPUTER: IBM PS/Z MODEL 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.1) CURRENT APPLICATION NUMBER: US/08/033,081B FILING DATE: MATCH 11, 193 CLASSIFICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 00/246/069005 FILING DATE: JANUARY 00/246/069005 REGISTRATION NUMBER: 00/246/069005 REGISTRATION NUMBER: 00/246/069005 REFERENCE/DOCKET NUMBER: 00/246/069005 TELEFORMUNICATION INFORMATION: TELEFORMUNICATION INFORMATION: TELEFORMUNICATION TORNAMION: TELEFORMUNICATION TELEFORMUNICATION TELEFORMUNICATION TELEFORMUNICATION TELEFORMUN	COMPUTER: IBM PS/2 Model 50Z or 55SX OPBRATING SYSTEM: MS-DOS (Version 5.1) SOFTWARE: WORDERFECT (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 1993 PRIOR APPLICATION APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/069005 TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-5070 TELEFAX: 6617) 542-8906 TELEFAX: 60154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear TOPOLOGY: linear S-08-033-081B-1	COMPUTER: IBM PS/2 Model 507 or 558X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WOTGDETFECT (Version 5.1) URRENT APPLICATION NUMBER: US/08/03,081B FILLING DATE: MARCH 11, 1993 CLASSIFICATION: 435 RIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/869,215 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY,AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELES: 200154 ORMATION FOR SEQ ID NO: 1: EQUIENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid	COMPUTER: IBM PS/2 Model 507 or 55X OPERATING SYSTEM: MS-DOS (Version 5.1) URRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILLING DATE: March 11, 1993 CLASSIFICATION LATA: RIOR APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 ELECHOMINICATION INFORMATION: TELLEPAN: (617) 542-8906 TELLEPAN: (617) 542-8906 TELLESA: 200154	COMPUTER: IBM PS/2 Model 507 or 55% OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordDerfect (Version 5.1) URRENT APPLICATION DATA: APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 1993 CLASSIFICATION: 435 RICA APPLICATION UNMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark, Paul T REGISTRATION UNMBER: 00,162 REFERENCE/DOCKET NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005	BM PS/2 Model 50% or 558x STEM: MS-DOS (Version 5.0) ordPerfect (Version 5.1) ATION DATA: NUMBER: US/08/033,081B MATCH 11, 1993 ON: 435 ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/825,296 January 24, 1990 INFORMATION: Paul T. NUMBER: 30.162	BM PS/2 Model 502 or 553x STEM: MS-DOS (Version 5.0) ordPerfect (Version 5.1) ATION DATA: NUMBER: US/08/033,081B March 11, 193 ON: 435 ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/469,215 January 24, 1990	UMBER OF SEQUENCES: 25 ORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804	OF INVENTION: DIAGNOSIS OF HEREDITARY OF INVENTION: DEGENERATIVE DISEASES R OF SEQUENCES: 25 SPONDENCE ADDRESS: SPONDENCE ADDRESS: ETS 15h & Richardson EET: 225 Franklin Street FE: Massachusetts TE: Massachusetts NTRY: U.S.A. 10 2110 - 2804	PLICANT: Dryja, Thaddeus P. PLICANT: Berson, Eliot L. PLICANT: Berson, Eliot L. PLICANT: Berson, Eliot L. PLEOF INVENTION: DIAGNOSIS OF HEREDITARY PLE OF INVENTION: DEGENERATIVE DISEASES MEER OF SEQUENCES: 25 MESPONDENCE ADDRESS: MARESPONDENCE ADDRES
COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: LBM PS/2 Model 502 or 555X COMPUTER: LBM PS/2 Model 502 or 555X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTMARE: MOTOPERFECT (VERSION 5.0) SOFTMARE: MS-DOS (VERSION 5.0) CURRENT APPLICATION NUMBER: US/08/033.081B FILING DATE: MARCH 11, 1993 APPLICATION NUMBER: 07/825,296 FILING DATE: MS-DOS (VERSION 5.2) APPLICATION NUMBER: 00/465,215 FILING DATE: JANUARY 23, 1992 APPLICATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELEFAX: (617) 542-8966 TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: TELEPHONE: 617) 542-8966 TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: LENGTH: 302 STRANDENNESS: double TODOLOGY: linear SCOPE: 11 SEQUENCE CHARACTERISTICS: LENGTH: 302 STRANDENNESS: double TODOLOGY: 11 SEQUENCE CHARACTERISTICS: LENGTH: 302 STRANDENNESS: double TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: LENGTH: 302 STRANDENNESS: double TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: LENGTH: 302 STRANDENNESS: double TYPE: DICLEIC SCI IN ON: 1: SEQUENCE CHARACTERISTICS: LENGTH: 302 STRANDENNESS: double TODOLOGY: 11 SEQUENCE CHARACTERISTICS: LENGTH: 302 STRANDENNESS: double TODOLOGY: 11 SEQUENCE CHARACTERISTICS: LENGTH: 302 STRANDENNESS: double TODOLOGY: 11 SEQUENCE CHARACTERISTICS: LENGTH: 302	COMPUTER READABLE FORM: MEDIUM TYPE: 35.7 Diskette, 1.44 Mb COMPUTER: IBM PS/Z Model 502 or 555X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WOODERFECT (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 00/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 00/469,215 FILING DATE: January 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 TELEGOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEFAX: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_BCCR: 124.50 QUALITY: 50.000 Percent Identity: 20.73 lignment_block: US-08-033-081B-1 from: 1 to: 301 Align seg 1/1 to: US-08-033-081B-1 from: 1 to: 301	COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/Z Model 502 or 555X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 00746/069005 FILING DATE: January 24, 1990 APPLICATION NUMBER: 00246/069005 FILING DATE: JANUARY 20, 162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-5070 TELEFAX: (617) 542-5070 TELEFAX: 1016 TYPE: DOLL-11 SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: DULL-12 acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lingment_scores: 1ignment_scores: 1ignment_block: US-08-033-081B-1	COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 502 or 558X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WGOTGPETECT (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION PATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELERX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: Nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_scores: Ouality: 124.50 Retio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.73	COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/825,296 FILLING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/069005 TELEFAN: (617) 542-5970 TELEFAN: (617) 542-5970 TELEFAN: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 STRANDEDNESS: double TOPOLOGY: linear TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear	OMPUTER READABLE FORM: MEDIUM TYPE: 3.5" DISkette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WordPerfect (Version 5.1) URRENT APPLICATION DATA: APPLICATION UNMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION UNMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 FILING DATE: JANUARY APPLICATION UNMBER: 00246/069005 FILING DATE: JANUARY APPLICATION UNMBER: 00246/069005 FILING DATE: JANUARY THE CHARACTEN 1 NFORMATION: TREEFRING DOCKET NUMBER: 00246/069005 TELECAMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 ORMATION FOR SEQ ID NO: 1: EQUIENCE CHARACTERISTICS: TELEPHORE: 3016 ORMATION FOR SEQ ID NO: 1: EQUIENCE CHARACTERISTICS: TYPE: nucleic acid	OMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: 1BM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WordPerfect (Version 5.1) URRENT APPLICATION DATA: APPLICATION NUMBER: US/08/03,081B FILLING DATE: March 11, 1993 CLASSIFICATION NUMBER: 07/825,296 FILLING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILLING DATE: January 24, 1990 TORNEY,AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/069005 ELECOMMUNICATION INFORMATION: REGISTRATION NUMBER: 0246/069005 ELECOMMUNICATION INFORMATION: TELEFAX: (617) 542-8906 TELEEX: 200154	OMPUTER READABLE FORM: MEDIUM TYPE: 3.5" DISkette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55X OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WordPerfect (Version 5.1) URRENT APPLICATION DATA: APPLICATION UNMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION UMBER: U5/08/233,081B FILING DATE: JOUNGER: U5/08/233,081B FILING DATE: JOUNGER: U5/08/233,081B FILING DATE: JOUNGER: U5/08/233,081B FILING DATE: JOUNGER: U5/08/23,081B	BLE FORM: 3.5 Diskette, 1.44 Mb 3.5 Diskette, 1.74 Mb BM PS/2 Model 502 or 55SX STEM: MS-ODS (Version 5.1) ATION DATA: NUMBER: US/08/033,081B March 11, 193 ON: 435 ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/469,215 January 24, 1990 INFORMATION: Paul T NUMBER: 30.162	JLE FORM: 3.5" Diskette, 1.44 Mb 3.5" Diskette, 1.74 Mb 3.5" Diskette, 1.74 Mb 3.5" Diskette, 1.74 Mb 3.5" Diskette, 1.74 Mb 80" MS-DOS (Version 5.0) FORDER FECT (Version 5.1) ATION DATA: NUMBER: U5/08/033,081B March 11, 1993 ON: 435 ON: 435 ON: 435 ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/469,215 January 24, 1990	UMBER OF SEQUENCES: 25 ORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston	OF INVENTION: DIAGNOSIS OF HEREDITARY OF INVENTION: DEGENERATIVE DISEASES OF INVENTION: DEGENERATIVE DISEASES SEQUENCES: 25 SPONDENCE ADDRESS: RESSEE: Fish & Richardson EET: 225 Franklin Street Y: Boston TE: Massachusetts	PLICANT: Dryja, Thaddeus P. PLICANT: Berson, Ellot L. PLE OF INVENTION: DIGENERATIVE DISEASES ABER OF SEQUENCES: 25 ABER OF SEQUENCES: 25 ADDRESSE: Fish & Richardson STREET: 25 Franklin Street LTY: Boston
COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READALE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READALE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READALE FORM: COMPUTER: LEM PS/2 Model 502 or 555X OPERATING SYSTEM: MS-DOS (Version 5.1) CURRENT APPLICATION DATA: APPLICATION UNMEER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION UNMEER: US/08/23,081B FILING DATE: January 21, 1990 APPLICATION UNMEER: US/07/855,296 FILING DATE: January 21, 1990 APPLICATION UNMEER: 00/469,215 FILING DATE: January 21, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00/246/069005 TELEPHONE: (617) 542-5970 TELERX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear 11gnment_Scores: 11gnment_Scores: 11gnment_Scores: 124.50 Ratio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.732 Lignment_block: US-09-510-332-1 x US-08-033-081B-1 11gnment_block: 11gnment_block: 11gnment_block: 12g-09-510-332-1 x US-08-033-081B-1 11gnment_block: 12g-09-510-332-1 x US-08-033-081B-1 11gnment_block: 13g-09-510-332-1 x US-08-033-081B-1 14gnment_block: 14g-09-510-332-1 x US-08-033-081B-1 14glilililililililililililililililililili	COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 5.0 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: MODEL SOR OF 5.50 SOFTWARE: MODEL MS-008 (Version 5.0) SOFTWARE: MOTOPECT (Version 5.0) SOFTWARE: Wordperfect (Version 5.0) PRICE DATE: January 23, 1993 APPLICATION NUMBER: 07/825, 296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/825, 296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/825, 296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 00/246/069005 FILING DATE: January 24, 1990 APP	COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORW: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: LBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: Wordperfect (Version 5.0) SOFTWARE: Wordperfect (Version 5.1) CURRENT APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 193 CLASSIFICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/865,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 TELEFOXION OF SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TYPE: 02411y: 124.50 RRALIO: 0.759 Percent Similarity: 50.000 Percent Identity: 20.73 Lignment_scores: 11gnment_scores: 07901032-1 x US-08-033-081B-1	COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORW: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: LBM PS/2 Model 50Z or 55SX OPERATING SYSTEM, MS-DOS (Version 5.0) SOFTWARE: Wordperfect (Version 5.0) SOFTWARE: Wordperfect (Version 5.1) CURRENT APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 193 CLASSIFICATION = 435 PRIOR APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1990 ATTONNEY/AGENT INFORMATION: NAME: Clarx, Paul T. REGISTRATION NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005 REFERENCE/TON INFORMATION: NAME: Clarx, Paul T. REGISTRATION FOR SEQ ID NO: 1: SEQUENCE CHARRCTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_scores: Ouality: 124.50 Retio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.73	COUNTRY: U.S.A. COUNTRY: U.S.A. CIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.47 Mb MEDIUM TYPE: MS-DOS (Version 5.0) OCHONDITER: ISH MS-DOS (Version 5.1) CORFENT APPLICATION DATA: APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 1993 PRIOR APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/89,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: NAME: Clark, Paul T. REGISTRATION SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1	COUNTRY: U.S.A. ZIP: 02110-2804 ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55X OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WOrdDerfect (Version 5.1) URRENT APPLICATION NUMBER: US/08/03,081B FILLING DATE: March 11, 1993 CLASSIFICATION: 435 RICHASTIFICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/869,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELES: 200154 ORMATION FOR SEQ ID NO: 1: EQUIENCE CHARACTERISTICS: ELENGTH: 3016 TYPE: nucleic acid	COUNTRY: U.S.A. ZIP: 02110-2804 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER EADABLE FORM: COMPUTER: IBM PS/2 Model 502 or 558X OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WordPerfect (Version 5.1) URRENT APPLICATION DATA: US/08/033,081B FILLING DATE: March 11, 1993 CLASSIFICATION LOATA: 435 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 ELECHOMINICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEX: 200154	COUNTRY: U.S.A. ZIP: 02110-2804 ZIP: 02110-2804 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READABLE FORM: COMPUTER: IBM PS/2 Model 502 or 555X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordDerfect (Version 5.1) URRENT APPLICATION DATA: APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 1993 CLASSIFICATION: 435 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/825,286 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: REGESTRATION UMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005	S.A. 2804 BLE FORM: BLE FORM: BLE FORM: 3.5" Diskette, 1.44 Mb 3.5" Diskette, 1.84 Mb 3.5" Diskette, 1.47 Mb BM PS/2 Model 502 or 555X STEM: MS-DOS (Version 5.0) ordberfect (Version 5.1) ATION DATA: NUMBER: US/08/033,081B March 11, 1993 ON: 435 ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/825,296 January 24, 1990 INFORMATION: Paul T. NUMBER: 30.162	S.A. 2804 BLE FORM: BLE FORM: 3.5" Diskette, 1.44 Mb BM PS/2 Model 502 or 555X STEM: MS-DOS (Version 5.0) ordPerfect (Version 5.1) ATION DATA: NUMBER: US/08/033,081B March 11, 193 ON: 435 ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/469,215 January 24, 1990	UMBER OF SEQUENCES: 25 ORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street	OF INVENTION: DISGNOSIS OF HEREDITARY OF INVENTION: DEGENERATIVE DISEASES R OF SEQUENCES: 25 SPONDENCE ADDRESS: SPONDENCE ADDRESS: EEST: 225 Franklin Street	PLICANT: Dryja, Thaddeus P. PLICANT: Berson, Eliot L. TLE OF INVENTION: DIAGNOSIS OF HEREDITARY PLE OF INVENTION: DEGENERATIVE DISEASES HER OF SEQUENCES: 25 ARESPONDENCE ADDRESS: ARRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson DDRESSE: Fish & Richardson
COMPUTE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READALE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READALE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READALE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IMP 8/2 Model 502 or 558X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTMARE: Mordberfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033/081B FILING DATE: MARCH 11, 1993 PRIOR APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELEPAX: (617) 542-8906 TELEPAX: (617) 542-8906 TELEPAX: 200154 INFORMATION FOR SEQ ID NO: 1: LENGTH: 3016 TELEPAX: 1015 TELEPAX: 1015 TELEPAX: 1016 TELEPAX: 1017 TELEPAX: 1016 TELEPAX: 1017 TELEPAX: 1016 TEL	CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 502 or 555x OPENATING SYSTEM: MS-DOS (Version 5.0) SOFTMARE: Wordperfect (Version 5.1) COURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: 30,162 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 FILESCOMMUNICATION NIMBER: 00246/069005 TELEFAX: (617) 542-5070 TELEFAX: (617) 542-5070 TELEFAX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_block: US-08-033-081B-1 Lignment_block: US-08-033-081B-1 from: 1 to: 301 Align seg 1/1 to: US-08-033-081B-1 from: 1	CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: LBM PS/2 Model 50% or 55% OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION NUMBER: US/08/03,081B FILING DATE: MATCH 11, 1993 CLASSIFICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELERX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: TELEPHONE: (617) 542-8906 TELERX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear 11gnment_scores:	CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50% or 55% OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION NUMBER: US/08/033.081B FILING DATE: March 11, 1993 CLASSIFICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00,246/069005 TELEFORMUNICATION INFORMATION: REFERENCE/DOCKET NUMBER: 00246/069005 TELEFORMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELEEX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_scores: Ouality: 124.50 Retio: 0.759 Percent Similarity: 50.000 Percent Identity: 20.73	CITY: BOSTON STATE: MASSACHUSELTS COUNTRY: U.S.A. COUNTRY: U.S.A. COUNTRY: U.S.A. COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 502 or 558X OPERATING SYSTEM: MS-DOS (VERSION 5.0 SOFTWARE: WASCADER FECT (VERSION 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 193 CLASSIFICATION 1435 PRIOR APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 00246/069005 TELEPHONE: (617) 542-5070 TELEPHONE: (617) 542-5070 TELEFAX: (617) 542-8906 TELEFAX: (617) 542-8906 TELEFAX: CHARACTERISTICS: LENGTH: 3016 STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1	COLTY: BOSTON STATE: MASSACHUSELTS COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WORDERFECT (Version 5.1) URRENT APPLICATION NUMBER: US/08/033,081B FILLING DATE: MATCH 11, 1993 CLASSIFICATION LOATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/869,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark, Paul T REGISTRATION NUMBER: 00246/069005 ELECOMMUNICATION INFORMATION: REPERNCE/DOCKET NUMBER: 00246/069005 ELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 TELES: 200154 ORMATION FOR SEQ ID NO: 1: EQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid	CITY: BOSTON STATE: MASSACHUSELTS COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDLUM TYPE: 3.5" DISKETTE, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WORDER: US/08/033,081B FILLING DATE: MATCH 11, 1993 CLASSIFICATION UNMBER: US/08/033,081B FILLING DATE: MATCH 11, 1993 CLASSIFICATION NUMBER: 07/825,296 FILLING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 ELECOMMUNICATION INFORMATION: REGISTRATION NUMBER: 00246/069005 ELECOMMUNICATION INFORMATION: TELEFAX: (617) 542-8906 TELLEX: 200154	COLTY: BOSTON STATE: MASSACHUSELTS COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDDIUM TYPE: 3.5" DISkette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WORDER: CONTROL (Version 5.1) URRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILLING DATE: MATCH 11, 1993 CLASSIFICATION LATA: APPLICATION NUMBER: 07/825,296 FILLING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILLING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: REGISTRATION UMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005	an Associated States of St	achusetts S.A. BLE FORM: BLE FORM: BLE FORM: 3.5" Diskette, 1.44 Mb BM PS/2 Model 502 or 555X STEM: MS-DOS (Version 5.0) ordPerfect (Version 5.1) ATION DATA: NUMBER: US/08/033,081B March 11, 1993 ON: 435 ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/469,215 January 24, 1990	UMBER OF SEQUENCES: 25 ORRESPONDENCE ADDRESS:	OF INVENTION: DIAGNOSIS OF HEREDITARY OF INVENTION: DEGENERATIVE DISEASES R OF SEQUENCES: 25 SPONDENCE ADDRESS:	PLICANT: Dryja, Thaddeus P. PLICANT: Berson, Eliot L. PLICANT: Berson, Eliot L. PLE OF INVENTION: DIAGNOSIS OF HEREDITARY PLE OF INVENTION: DEGENERATIVE DISEASES ### ABER OF SEQUENCES: RESPONDENCE ADDRESS:
ADDRESSEE: Fish & Bichardson STREET: 225 Franklin Street CITY: Boston CITY: Boston Assachusetts COUNTRY: U.S.A. STREET: 275 Franklin Street STATE: Massachusetts COUNTRY: U.S.A. COUNTRY: U.S.A. LENGTH: Massachusetts COUNTRY: U.S.A. COMPUTER: SISH PS/2 Model 50? Or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) COURDENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION NUMBER: US/08/033,081B FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/469,215 APPLICATION NUMBER: 07/469,216 APPLICATION NUMBER: 07/469,216 APPLICATION NUMBER: 07/469,216 APPLICATION NUMBER: 0	ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 5.0 SOFTWARE: MAS-DOS (Version 5.0) SOFTWARE: MAS-DOS (Version 5.1) CURRENT APPLICATION NUMBER: US/08/033,081B FILING DATE: MATCh 11, 1993 CLASSIFICATION UMBER: 07/825,296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 007469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 TELEGOMMUNICATION INFORMATION: TELEPHONE: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: NUCLEIC acid STRANDEDNESS: double TOPOLOGY: linear 19-08-033-081B-1 Lignment_Bock: US-08-033-081B-1 Lignment_block: US-08-033-081B-1 Alignment_block: US-08-033-081B-1 from: 1 to: 301	ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 5.0 SOFTWARE: HEM PS/2 Model 502 or 555X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: HEM PS/2 Model 502 or 555X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/869,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECOMMUNICATION INFORMATION: REGISTRATION: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 TYPE: NUCleic acid STRANDEDNESS: double TOPOLOGY: linear Is-08-033-081B-1 Length: 32 Percent Similarity: 50.000 Percent Identity: 20.73 lignment_Scores: 011910-033-081B-1 LENGTH: 302-08-033-081B-1	ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Liskette, 1.44 Mb COMPUTER: LIBM PS/2 Model 502 or 558X OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WOrdPerfect (Version 5.0) SOFTWARE: WORDPERCATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION DATA: APPLICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 APPLICATION NUMBER: 007/469,215 APPLICATION NUMBER: 00	ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER READABLE FORM: MEDIUM TYPE: MS-DOS (Version 5.0 SOFWMARE: WordPerfect (Version 5.0 SOFWMARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION: 435 PRIOR APPLICATION NUMBER: 07/825,296 FILLING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: CLARK, PAUL T. REGISTRATION NUMBER: 00246/069005 TELEFAX: (617) 542-8906 TELEFAX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 STRANDEDNESS: double TOPOLOGY: linear TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear	ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER: READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: Wordperfect (Version 5.0) URRENT APPLICATION DATA: APPLICATION NUMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/869,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION UMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 FILEWOMNICATION TORNATION: TELEPHONE: (617) 542-8906 ORMATION FOR SEQ ID NO: 1: EQUIENCE CHARACTERISTICS: LENGTH: 3016 TYPE: nucleic acid	ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) COMPUTER: IBM PS/2 MODEL 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.1) URRENT APPLICATION NOTA: APPLICATION NUMBER: US/08/033,081B FILLING DATE: March 11, 1993 CLASSIFICATION NOTA: APPLICATION NUMBER: 07/825,296 FILLING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILLING DATE: January 24, 1990 TTORNEY,AGENT INFORMATION: REGISTRATION NUMBER: 00246/069005 ELECOMMUNICATION INFORMATION: REGISTRATION NUMBER: 0246/069005 ELECOMMUNICATION INFORMATION: TELEPAN: (617) 542-8906 TELLEX: 200154	ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Wassachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER: READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0 SOFTWARE: WORDPERFECT (Version 5.0) COFTWARE: WORDPERFECT (Version 5.1) URRENT APPLICATION DATA: APPLICATION UNMBER: US/08/033,081B FILING DATE: March 11, 1993 CLASSIFICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 TTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION UMBER: 00246/069005 REFERENCE/DOCKET NUMBER: 00246/069005	Fish & Richardson Franklin Street achusetts S.A. 2804 BLE FORM: BLE FORM: BLE FORM: BY/2 Model 50Z or 555X STEM: MS-DOS (Version 5.0) CORDPERFECT (Version 5.1) ATION DATA: NUMBER: US/08/033,081B March 11, 193 ON: 435 ON: 435 ION DATA: NUMBER: 07/825,296 January 23, 1992 NUMBER: 07/825,296 January 24, 1990 INFORMATION: Paul T. NUMBER: 7,469,215 January 24, 1990 INFORMATION: Paul T. NUMBER: 30.162	Fish & Richardson Franklin Street achusetts S.A. 2804 BLE FORM: BLE FORM: 3.5" Diskette, 1.44 Mb 3.5" Diskette, 1.84 Mb Cordberfect (Version 5.1) ATION DATA: NUMBER: US/08/033,081B March 11, 1993 ON: 435 O		OF INVENTION: DEGENCERATIVE DISEASES	THE OF INVENTION: DEGENERATIVE DISEASE LICANT: Berson, Eliot L. PRESON DIAGNOSIS OF HEREDITARY LE OF INVENTION: DIAGNOSIS OF HEREDITARY
PREBRIC NO. 5499521 GRNERAL INFORMATION: GRNERAL INFORMATION: APPLICANT: Berson, Eliot L. TITLE OF INVENTION: DIGGSERRATIVE DISBASES NUMBER OF INVENTION: DECEMERATIVE DISBASES NUMBER OF INVENTION: DECEMERATION STREET: 225 FRANKLIN Street CITY: Boston STATE: MASSACHUSETTE COUNTER: MASSACHUSETT COUNTER: MASSACHUSETT COUNTER: MASSACHUSETT COUNTER: MASSACHUSETT COUNTER: MASSACHUSETT COUNTER: MASSACHUSETT COUNTER: MASSACHUSET COUNTE	PATENT NO. 5498511 GENERAL INFORMATION: APPLICANT: Berson, Ellot L. TITLE OF INVENTION: DEGENERATIVE DISEASES CORRESPONDENCE ADDRESS: ADDRESSEE: 1916 A RICCHARISON STREET: 225 FRANKLIN Street CITY: BOSTON STREET: 225 FRANKLIN STREET COUNTRY: U.S.A. ZIP: 0210-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" DISKETLE, 1.44 Mb COMPUTER SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WORDER: WS-DOS (Version 5.0) SOFTWARE: WORDER: US-08/033,081B FILING DATE: MARCH 11, 1993 CLASSIFICATION NUMBER: US-08/033,081B FILING DATE: MARCH 11, 1993 CLASSIFICATION NUMBER: 07/825,296 FILING DATE: January 23, 1992 APPLICATION NUMBER: 07/469,215 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELEPHONE: (617) 542-8906 TELEPHONE: (617) 542-8906 TELEPHONE: (617) 542-8906 TELEPHONE: ONLY 11 STRANDENESS: double TOPOLOGY: linear S-08-033-081B-1 Lignment_scores: US-08-033-081B-1 Lignment_scores: Alignment_block: US-08-033-081B-1 from: 1 to:	PATENT NO. 5498521 GENERAL INFORMATION: APPLICANT: Berson, Ellot L. TITLE OF INVENTION: DEGENERATIVE DISEASES NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.1) CURRENT APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 1993 CLASSIFICATION UNMBER: US/08/03,081B FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/825,296 APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/825,296 APPLICATION NU	PATENT NO. 5498521 GENERAL INFORMATION: APPLICANT: Dryja, Thaddeus P. APPLICANT: Berson, Ellot L. TITLE OF INVENTION: DEGENERATIVE DISEASES NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE; Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATION, SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 193 CLASSIFICATION NUMBER: 07/825,296 FILING DATE: January 24, 1990 APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1992 APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1992 APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1992 APPLICATION NUMBER: 00246/069005 TELECOMMUNICATION THORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELECANS (617) 542-8906 TELEFAX: 200154 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 STRANDEDNESS: double TOPOLOGY: linear Is-08-033-081B-1 Lignment_scores: Ouality: 124-50 Percent Similarity: 50.000 Percent Identity: 20.000	PATENTIAL INFORMATION: APPLICANT: Dryja, Thaddeus P. APPLICANT: Dryja, Thaddeus P. APPLICANT: Berson, Ellot L. TITLE OF INVENTION: DEGENERATIVE DISEASES NUMBER OF SEQUENCES: 25 CORRESPONDENCE ADDRESS: ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street CITY: Boston STATE: Massachusetts COUNTRY: U.S.A. ZIP: 02110-2804 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM PS/2 Model 50Z or 55SX OPERATING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/03,081B FILING DATE: March 11, 193 CLASSIFICATION NUMBER: 07/825,296 APPLICATION NUMBER: 07/825,296 FILING DATE: January 24, 1990 ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T. REGISTRATION NUMBER: 30,162 REFERENCE/DOCKET NUMBER: 00246/069005 TELEPHONE: (617) 542-8906 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 3016 STRANDEDNESS: double TOPOLOGY: linear S-08-033-081B-1	LICANT: DPYLOUGH OF YOUR SAULT REPORTATION: ALL INFORMATION: BLIGHT L. PLICANT: Dryja, Thaddeus P. PLICANT: Dryja, Thaddeus P. PLICANT: BETSON, ELIOT L. RESPONDENCE ADDRESS: DDRESSES: FISH & RICHARDSON STREET: 225 FRANKIN STREET LITY: BOSTON TATE: MASSACHUSETTS DOUTRY: U.S.A. 11P: 02110-2804 PUTER READABLE FORM: FOUNTRY: U.S.A. PUTER READABLE FORM: FEDIUM TYPE: 3.5" DISKETTE, 1.44 Mb SOMPUTER: IBM PS/2 Model 50Z or 55SX PERATING SYSTEM: MS-DOS (VETSION 5.1) REPUTEATION NUMBER: US/08/03,081B TLING DATE: MARCH 11, 1993 TLING DATE: MARCH 11, 1993 TLING DATE: JANUARY 23, 1992 PPLICATION NUMBER: 07/825,296 TLING DATE: JANUARY 24, 1990 TORNEY/AGENT INFORMATION: AME: Clark, Paul T. EGISTRATION NUMBER: 00246/069005 ECOMMUNICATION INFORMATION: ELEPEAX: (617) 542-8906 ELEX: 200154 MATION FOR SEQ ID NO: 1: ENGINE : Gold ALCHARACTERISTICS: ENGINE: DIGLEI CALID VEEL CLAICA COLOR MATION FOR SEQ ID NO: 1: ENGINE : 101616 acid	LNG. 5498521 LNG. 5498521 LICANT: Dryja, Thaddeus P. PLICANT: Berson, Eliot L. THE OF INVENTION: DEGENERATIVE DISEASES ABER OF SEQUENCES: 25 ARRESPONDENCE ADDRESS: LDDRESSEE: Fish & Richardson STREET: 225 Franklin Street LTY: Bassachusetts DOUNTRY: U.S.A. JIP: 02110-2804 PUTER READABLE FORM: PUTER READABLE FORM: PUTER READABLE FORM: PUTER SYSTEM: MS-DOS (Version 5.0) DOFTWARE: WordPerfect (Version 5.0) DOFTWARE: WordPerfect (Version 5.1) RENT APPLICATION NUMBER: US/08/033,081B LING DATE: January 23, 199 PPLICATION NUMBER: 07/825,286 TLING DATE: January 23, 1990 ORNEY/AGENT INFORMATION: MAE: Clark, Paul T. MAE: Clark, Paul T. BLEPHONE: (617) 542-8906 ELEPAN: (617) 542-8906 ELEPAN: (617) 542-8906 ELEPAN: (617) 542-8906 ELEPAN: (617) 542-8906	L NO. 5498521 L NO. 5498521 ALL INFORMATION: BLICANT: Dryja, Thaddeus P. PLICANT: BETSON, ELIOT L. PLICANT: BESTSON BARESPONDENCE ADDRESS: ADDRESSS: ADDRESSS: ADDRESSS: LAST Fish & Richardson STREET: 25 Franklin Street STATE: Massachusetts COUNTRY: U.S.A. PUTER READABLE FORM: PUTER SYSTEM: MS-DOS (Version 5.0) PERATTING SYSTEM: MS-DOS (Version 5.0) PERATTING SYSTEM: MS-DOS (Version 5.1) RENT APPLICATION DATA: PPLICATION NUMBER: US/08/03,081B ILING DATE: MARCH 11, 1993 LASSIFICATION NUMBER: 07/825,296 TILING DATE: January 23, 1992 PPLICATION NUMBER: 07/469,215 TILING DATE: January 24, 1990 ORNEY/AGENT INFORMATION: BARE: Clark, Paul T. EGESTRATTON NUMBER: 00246/069005 EEGESTRATTON NUMBER: 00246/069005	LNG. 5498521 LNG. 5498521 LLICANT: Dryja, Thaddeus P. PLICANT: Berson, Ellot L. PEGENERATIVE DISEASES ABER OF SEQUENCES: 25 ABER OF SEQUENCE ADDRESS: ADDRESSE: 25 Franklin Street ITY: BOSTON TATE: Massachusetts COUNTRY: U.S.A. PUTER READABLE FORM: PUTER READABLE FORM: PUTER SYSTEM: MS-2 Model 50Z or 55SX PERATING SYSTEM: MS-DOS (Version 5.0) PERATING SYSTEM: MS-DOS (Version 5.1) REMY APPLICATION DATA: (Version 5.1) PERATICATION NUMBER: US/08/03,081B "LIANG DATE: MARCH 11, 1993 LASSIFICATION NUMBER: 07/825,286 "LING DATE: January 24, 1990 ORNEY/AGENT INFORMATION: MAME: Clark, Paul T. EGISTRATION NUMBER: 30.162	ENG. 5498521 ENG. 5498521 LICANT: Dryja, Thaddeus P. PLICANT: Berson, Eliot L. PLICANT: Berson, Eliot L. DEGEMERATION: DEGEMERATIVE DISEASES BER OF SEQUENCES: 25 BERNESSEE: Fish & Richardson STREET: 225 Franklin Street LITY: BOSTON STREET: BASSACHUSETTS LOUNTRY: U.S.A. 10: 02110-2804 PUTER READABLE FORM: #PUTER READABLE FORM: #BOUNT TYPE: 3.5" Diskette, 1.44 Mb COMPUTER: IBM FS/2 Model 50Z or 555X DERARTING SYSTEM: MS-DOS (Version 5.0) SOFTWARE: WordPerfect (Version 5.0) SOFTWARE: WordPerfect (Version 5.1) RERNT APPLICATION DATA: LASSIFICATION UNWBER: US/08/03,081B "LING DATE: March 11, 193 "LANGERICATION UNWBER: US/08/23,081B "LING DATE: March 11, 193 "LENGLATION UNWBER: US/08/33,081B "LING DATE: January 24, 1990 "LING DATE: January 24, 1990	E NO. 5498521 RAL INFORMATION: PILCANT: Dryja, Thaddeus P. PILCANT: Dryja, Thaddeus P.	L NO. 5498521	

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-820-521-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application Patent No. 5942416
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,521
FILING DATE: 19-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: CDNA CLONE HNFDY20 THAT ENCODES
TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
APPLICANT:
                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 CTTTCTG...CGGCTTGCGTTTCGCGTCGCTTTTTTTTCGCTGGTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  245 lPheLeuSerSerLeuLysPheHisIleArgArgPhe...IlePheLeup 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 hrIleGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAla 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 lySerArgValProGlyArgClyAlaProIle.....SerAlaLeuLeu 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    586 CTGTG.....GTTGGCTTTTGCTTTTTTTTTTCTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Han, William T
REGISTRATION NUMBER: 34,344
                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTCTTCTGTGTTGTCTTTTTTTTTTTTTTTCT.....TTGCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hePheIleLeuVal 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysVa 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTTTTGCTTGTT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ePheSerLeuGlyArgHisThrArgGlnMetArgAsnThrVal...AlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ......LeuArgLysPhePheSerGlnAsnAlaT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08820521
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bergsma, Derk
Ganesh, Sathe
Fuetterer, Wendy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552
```

```
alignment_block:
us-09-510-332-1 x us-08-820-521-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-820-521-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: US-08-820-521-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1841 base pairs
                                                                                                                    160 eSerGlnAsnAlaThrIleGln.....LysGluAspThrLeuAlaI 174
                                                                                                                                                                                                     144 HisSerLysTyrAlaGlyPheMetValProTyrPheLeuArgLysPhePh 160
                                                                                                                                                                                                                                                720 CTGCTCACTGCAGCGTGGTCTACGTCATAGAATTCTCAGGGGACATCTCC
                                                                                                                                                                                                                                                                                                 132
                                                                                                                                                                                                                                                                                                                             626
                                                                                                                                                                                                                                                                                                                                                                                                                                      106 LysValAlaSerValArgHisProLeuPheIleTrpLeuLysMetArg.. 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535 CCTGCCCTTCATCCTCTGCCCACTCTCTGGA.....TTCATCTTCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               485 CTGTTCCTGCCTTTCCGCATGGTGGAGGCAGCCAATGGCATGCACTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 GCTGGCCCTGGTGGTCTTCGTGGGCAAGCTGCAGCGCCGCCCGGTGGCC. 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 TTCTCGGTGTACCTTCTCACTTTCCTGGTGGGGCTCCCCCTCAAC...CT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: GITELECOMMUNICATION INFORMATION.
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 LeuPheIlePheTyrValAsnValIleValIle.....phePh 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 roLeuAspLeuLeuSerCysLeuAlaValSerArgIlePheLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26 eIleValValAsnGlyIleAspLeuIleLysHisArgLysMetAlaP 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 PheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIl 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 610-270-4026
TCCTCCTGCCGTGCGGCTGGAGATGGCTGTGGTCCTCTTTGTGGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCACCATCTATCTC...ACCGCCCTCTTCCTGGCAGCTGTGAGCATTGAA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eIleGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleA 89
                                       le.....GlnIlePheSerPheValAlaGluPheSerValPro 186
                                                                                                                                                                                                                                                                                   ly......SerLeuLeuTyrValSerMetIleCys.....ValPhe 143
                                                                                                                                                                                                                                                                                                                                                                       CGCTTCCTGAGTGTGGCCCACCCCCTG....TGGTACAAGACCCGGCC 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    snGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAla 105
                                                                              .GGCACCAATGGGACCTGCTACCTGGAGTTCCGGAAGGACCAGCTAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..GTGGACGTGCTCCTGCTCAACCTGACCGCCTCGGACCTGCTGCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122.50
0.833
49.662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GH50011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296
18
23.986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1841
                                                                                                                                                                                                                                                   769
                                                                                                                                                                                                                                                                                                                                 719
                                                                              827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59
```

<pre>seq_documentation_block: Sequence 20, Application US/08770379</pre>
seq_name: /cgn2_6/ptodata/2/1na/5B_COMB.seq:US-08-770-379-20
244 LysValPheLeuSerSerLeuLysPheHisIleArgArg 256
227 euLeuSerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIle 243
787 GAAGGTAAGGGGG
150 PheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIl 166
14 61
110 ValargHisProLeuPheIlerrpLeuLysMetAr 121
76 eMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluL 93 :::
60 LeupheIlePheTyrValAsnValIleValIlePhePheIleGluPheIl 76 ::: ::: ::::: :::::: 338 ATATCTCTATTGGCAGAAGTGTTGATGTTTTTGTTTCCCAATAT 381
43 roleuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePheLeuGln 59 :::: ::: :::: 288 CGATAGATAFACTGCTCCTGGGTATCTGCCTAAACTCGCTGTGTCTTAGC 337
27 eValValValAsnGlyIleAspLeuIleLysHisArgLysMetAlaP 43 :::: :::
11 LeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIleIl 27 ::: ::::: :::::
Align seg 1/1 to: US-08-728-603-16 from: 1 to: 1202
alignment_block: US-09-510-332-1 x US-08-728-603-16

```
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATICS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/770,379
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52342
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 32207 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-770-379-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-510-332-1 x US-08-770-379-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-08-770-379-20 from: 1 to: 32207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
Percent Similarity:
24362 NTATCTCTA.....TTGGCAGAAGTGTTGATGTTTTTGTTTCCCAATAT 24405
                                                                                                                                                                           24312 CGATAGATATACTGCTCCTGGGTATCTGCCTAAACTCGCTGTGTCTTAGC 24361
                                                                                                                                                                                                                                                                                                                                                         24274 CACCTACATT.....TTTTGCAAGCACCGATCGCGGGCAGGAG 24311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                      76
                                                                                                                              60 LeuPheIlePheTyrValAsnValIleValIlePhePheIleGluPheIl 76
                                                                                                                                                                                                            43 roLeuAspLeuLeuSerCysLeuAlaValSerArgIlePheLeuGln 59 :::||||::||
                                                                                                                                                                                                                                                                                            27 eValValAsnGlyIleAspLeuIleLysHisArgLysMetAla...p 43 :::: ||||||||||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chang, Yuan
APPLICANT: Bohenzky, Roy A.
APPLICANT: Russo, James J.
APPLICANT: Edelman, Isidore S.
APPLICANT: Edelman, Isidore S.
APPLICANT: Moore, Patrick S.
TITLE OF INVENTION: POLYEPPTIDES FROM KAPOSI'S SARCOMA-ASSOCIATED
TITLE OF INVENTION: HERPESVIRUS, DNA ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
                            eMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluL 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120.50
0.867
52.852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 263
Gaps: 14
Percent Identity: 22.433
```

	A.P.	
	FICATION: 435	
	APPLICATION NUMBER	
	SOFTWARE:	
	COMPUTER: IBM Com OPERATING SYSTEM:	
	MEDIUM TYP	
	ZIP: 02110-2804	
	STATE: COUNTRY	
	CITY: Boston	
	NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS:	
	TITLE OF INVENTION: RECE	
	Patent No. 5856124 GENERAL INFORMATION:	
	<pre>seq_documentation_block: ; Sequence 1, Application US/08466103A</pre>	
	seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-466-103A-1	
	24869 TACCACGTACTAAATCTACTGGACACTCTGCTAAGGCGA 24907	
	244 LysValPheLeuSerSerLeuLysPheHisIleArgArg 256	
24868	24824GTGATTGTTGCTGTGGTGCTGCTGTTTTTTGTGTTTTGCCTTCCCT	
243	227 euLeuSerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIle	
24823	24811 GAAGGTAAGGGGG	
227		
210	24761 TATGCTCTCACCTGGTGTGTGTGAGGAGGACAAAGCTGCAAGCCAGGCG	
6	100	
198	182 luPheSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIle	
c	:::	
100	166 eGlnLvsGl	
99		
24634		
149	138 erMetIleCysValPheHisSerLysTyrAlaGly	
24584	24539AAGCAGTCCCTCGGATGGGTACTGACATCCGCTGCACTGTTAATTG	
38	121 gIleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValS	
24538		
	ValArgH{sproleuphelle	
109	93 euTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSer ::: ::::: ::: 24444 ACTATTTATATGTCTACTTGGATATCTTCAGTGTTGTGTGTG	

```
NAME/KEY: Coding Sequence;
LOCATION: 32...1291
OTHER INFORMATION:
US-08-466-103A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-OCT-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/261,857

FILING DATE: 17-JUN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00786/250002

TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070

TELEFAX: 617/542-5070

TELEFAX: 617/542-8906

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-510-332-1 x US-08-466-103A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-466-103A-1 from: 1 to: 1320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 CCTGGGC......TTGTCTG
                                                                                                                                                                                                                                                                  101 ValPheTyrCysAlaLysValAlaSerValArgHisProLeuPheIleTr 117
                                                                                                                                                                                                                                                                                                                   351
                                                                                                                                                                                                                                                                                                                                                                                                   301 CATAGCTATTTTCCAGAATGGATGGACGCTTGGAAATATCCATTGTCAGA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 TCCTGAGGAACAAGAAGCTGCAGAATGCTGGAAATCTCTTTGTTGTCAGT 250
                                                                                                                                            436 CCACAGCCTGAGATATGACAAGCTTTATAATCAAAGAAGCACCTGGTGCT 485
                                                                                                                                                                               117 pLeuLysMetArgIleSerLysLeuVal......ProTrpMetI 130
                                                                                                                                                                                                                            386 TCAGTCTTCAACATAACAGCCATAGCTATCAACAGGTATTGCTACATCTG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 uLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleAspL 35
                                                                                               130 leLeuGlySerLeuLeuTyrValSerMetIleCysValPheHisSerLys 146
                                                                                                                                                                                                                                                                                                                                                                                                                                       67 lileValllePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51 LeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 eulleLysHisArgLysMetAlaProLeu...AspLeuLeuLeuSerCys 50
                    147
                                                                                                                                                                                                                                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 LeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLe 18
                                                                                                                                                                                                                                                                                                              TCAGTGGCTTCCTGATGGGACTCAGCGTT.....ATTGGA 385
                                                                                                                                                                                                                                                                                                                                         leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly 100
TyrAlaGlyPheMetVal.....
:::::||| :::
                                                            ACCTTGGCCTGACATGGATACTAACTATAATTGCAATCGTGCCAAACTTT 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118.00
0.752
53.401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wength: 294
Gaps: 12
Percent Identity: 19.388
    .ProTyrPheLeuArgLysPhePheSe 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 200
```

•		•					
FILING DATE: 05-Jul-1993 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Mitchard, Leonard C. REGISTRATION UNBER: 29.009 REFERENCE/DOCKET NUMBER: 47-80 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-816-4100 TELEPHONE: 703-816-4100 INFORMATION FOR SEO ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 8920 base pairs TYPE: nucleic acid	ADDRESSE: Nixon ADDRESSE: 1100 No. CITY: Arlington CITY: Arlington STATE: Virginia COUNTRY: USA ZIP: 22201-474 ZIP: 22201-474 COMPUTER READABLE F MEDIUM TYPE: Flo MEDIUM TYPE: Flo COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patent CURRENT APPLICATION APPLICATION UNBE FILL DATE: 06-	seq_documentation_block: Sequence 1, Application US/08446855A Patent No. 5849573 GENERAL INFORMATION: APPLICANT: Stewart, Thomas S APPLICANT: Flores, Maria V APPLICANT: O'Sullivan, William J TITLE OF INVENTION: Nucleotide sequence encoding carbamo) TITLE OF INVENTION: phosphate synthetase II NUMBER OF SEQUENCES: 2 COMMERCE ADDRESS:	46 127 me:	ച് ര ര ·	AAAGTTGACACAAACAGACTTGAGAAATTTCTTGACCAT	95	536 TTTGTTGGATCACTACAGTATGACCCCAGGATTTTTCCTTGCACATTTGC 585 161 rGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheS 178 :

. 206 gGlnMetArgAsnThrValAlaGlySerArgValProGlyArgGlyAlap	192PheAlaValLeuLeuLeuIlePheSerLeuGlyArgHisThr/ ::: ::: ! 6042 GAACAATTCATATTAATATTATATTCATCATTTAAATTTTCG	~ . ~	 156 TTTAAACGATTATAATGTTTGTATGTATGATCCATATTTTTTCA. 163 nAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheSer	CysvalPhe CTCTCATTT 	.23 rLysLeuValProTrpMetIleLeuGlySerLeuLeuT 	107 ValAlaSerValArgH1sProLeuPheIleTrpLeuLysMetArgIleSe	90 uLeuGlu.LeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLys ::::::: ::::::::::::::::::::: :::: 6293 TTTTTCCCTTATTTTTTCCATATTTTTTCTTTATTTTTTT	74 GluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGl ::::: ::: :::	66 SNV81I16ValIlePhePheIle :::	52 aValSerArgllePheLeuGlnLeuPheIlePheTyrValA ::: ::: ::: 6434 AATATATATCATTTTCATCTTCATAATATTCTTTTTTATTTATTTATCATC	36 IleLysH1sArgLysMetAlaProLeuAspLeuLeuLeuSerCysLeuAl :::	\rAsnGlyIleIleValValA 	4 SerHisLeuIle.IleTyrPheLeuLeuAlaValIleGlnPheLeuLeuG	Align seg 1/1 to reverse of: US-08-446-855A-1 from: 1	uS-09-510-332-1 x US-08-446-855A-1/rev	lignment_scores: Quality: 106.00 Length: 350 Ratio: 0.697 Gaps: 17 Percent Similarity: 43.429 Percent Identity: 20.857	; STRANDEDNESS; single ; TOPOLOGY: Linear ; MOLECULE TYPE; genomic US-08-446-855A-1
--	--	-------	---	-----------------------------------	--	--	--	---	----------------------------------	--	---	---------------------------	--	---	--	---	--

```
; NAME/KEY:
; LOCATION:
US-08-056-200-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-510-332-1 x US-08-056-200-93/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-08-056-200-93 from: 1 to: 9551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7347 CTGACGGCGGAGCTGCTGCTCCTCTTCGCGGAATTTTCTGTCACGCTCTT 7298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7203 CTGGCGGCGCAGCTGCGGGTTCCTCCAGGGAATTTTCTGTCACGCTCTT 7154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7297 GGCGGCGCAGCTGCTGTTCCTCCCCTTCCTGGAGCAGCTGTTCCTCTTCA 7248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7103 CGGAATTTTCTGTCCTCCTGCCGCAGCTGTTGTTGGCCCCTCCTGGCGGCG 7054
                                                                                                                                                   6916 CGCGGAATTTTCTGTCACGGTCCTGACGCCGCTGTTGCCCGCGCTCCTGG 6867
                                                                                                                                                                                                                          6936 CTGGCGCAGCTG.....TTCCTCCT 6917
                                                                                                                                                                                                                                                                                                    6971 CG.....CTCTTGGCGGCTCAGCTGCTGTTCCTCCCTCTC 6937
                                                                                                                                                                                                                                                                                                                                                                               7005 ......CACTTTCTGTTCCTCTAAACGGAATTTTCTGTCA 6972
                                                                                                                                                                                                                                                                                                                                                                                                                                                          7053 CAGCTGCTGCTCCTCCATGAATTTTCTCTCTTGTTCCTGGCGGCG.. 7006
6816 GTGCAGCTGCTGCTCCTCGAGGAATTTTCTCTCTGGTTCCTGACTGC 6767
                                                                                                                                                                                                                                                            140 IleCysValPheHisSerLysTyrAlaGlyPheMetValProTyrPheLe 156
                                                                                                                                                                                                                                                                                                                             123 erLysLeuValProTrpMetI1eLeuGlySerLeuLeuTyrValSerMet 139
                                                                                                                                                                                                                                                                                                                                                                                                                  106 sValAlaSerValArgHisProLeuPheIleTrpLeuLysMetArgIleS 123
                                                                      156 uArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThrLeuA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 LysMetAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIl 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 hrAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArg 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 uLeuAlaValIleGlnPheLeu.....LeuGlyIlePheT 23
                      190 PheLeuPheAlaValLeuLeuIlePheSerLeuGlyArgHisThrAr 206 ::: |||||||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 GluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLy 106 :::||| ::: |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 leGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsn 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 LeuGluSerHisLeuIleIleTyrPhe.....Le 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
1645..2511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
1507..1644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
2512..8070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 106.00
: 0.774
: 49.458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 7
Percent Identity: 23.827
```

; FEATURE: NAME/KEY: intron ; LOCATION: 16452511 ; FEATURE:	
; NAME/KEY: CDS; LOCATION: 15071644	
TYPE	
; INFORMATION FOR SEQ ID NO: 93: ; SEQUENCE CHARACTERISTICS:	
(714) 760-9502	
CATION INFORMATION:	
BER: 36	
. Ę	
LICATION N	
; CLASSIFICATION: 424 ; PRIOR APPLICATION DATA:	
4 5	
ATION DATA:	
SYSTEM: PC-DOS/MS-DOS	
TYPE: Flor	
; ZIP: 9266U : COMPUTER READABLE FORM:	
TRY	
ITY: Newport Beach	
ADDRESSEE: Knobbe, Martens, Olson & Bear	
NUMBER OF SEQUENCES: 117 CORRESPONDENCE ADDRESS:	
TITLE OF INVENTION: Mehods of Using Same	
Park, San	
APPLICANT: Chung	
APPLICANT: Lee, Seung-Chul	
. APPLICANT: Steinert, Peter M.	
quence tent No	
<pre>seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-800-644-93</pre>	
CTC	
N	
ឲ្ម	
240 Hi	
223 rolleSerAlaLeuLeuSerIleLeuSerPheLeuLteLeuTyrrneset 225 rolleSerAlaLeuLeuTerIleUSerPheLeuLteLeuTyrrneset 225 rolleSerAlaLeuLeuTyrrneset 225 rolleSerAlaLeuLeuTyrneset 225 rolleSerAlaLeuLeuTyrneset 225 rolleSerAlaLeuLeuTyrneset 225 rolleSerAlaLeuLeuTyrneset 225 rolleSerAlaLeuLeuLeuTyrneset 225 rolleSerAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuL	
<pre>gGlnMetArgAsnThrValAlaGlySerArgValProGlyArgG :::</pre>	

```
alignment_block:
US-09-510-332-1 x US-08-800-644-93/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY:
; LOCATION;
US-08-800-644-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-08-800-644-93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                         6916 CGCGGAATTTTCTGTCACGGTCCTGACGCCGCTGTTGCCCGCGCTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                             6936 CTGGCGCAGCTG......6917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6971 CG......CTCTTGGCGGCTCAGCTGCTGTTCCTCCCTCTC 6937
                                                                                                                                                                                                                                                                                         173 laIleGlnIlePheSerPheValAlaGluPheSerValProLeuLeuIle 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7153 GCCGGTGCAGCTGCTGCTTCCCTTTCCTGGAGCAGCTGTTCGTCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7053 CAGCTGCTGCTCGTCCATGAATTTTCTCTCTTGTTCCTGGCGGCG.. 7006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7103 CGGAATTTTCTGTCCTCCTGGCGCAGCTGTTGTTGGCCCTCCTGGCGGCG 7054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7203 CTGGCGGCGCAGCTGCGGGTTCCTCCTCGAGGAATTTTCTGTCACGCTCTT
                                                                                                                                                                                                                                                                                                                                                                                  156 uArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThrLeuA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 IleCysValPheHisSerLysTyrAlaGlyPheMetValProTyrPheLe 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 erLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSerMet 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7297 GGCGGCGCAGCTGCTGTTCCTCCCCTTCCTGGAGCAGCTGTTCCTTCTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7347 CTGACGGCGGAGCTGCTGTTCCTCTTCGCGGAATTTTCTGTCACGCTCTT 7298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 sValalaSerValArgH1sProLeuPheIleTrpLeuLysMetArgIleS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 ePheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 uLeuAlaValIleGlnPheLeu.....LeuGlyIlePheT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 LeuGluSerHisLeuIleIleTyrPhe.....Le 11
rolleSerAlaLeuLeuSerIleLeuSerPheLeuIleLeuTyrPheSer 239
                                                                                                                                                                                      PheLeuPheAlaValLeuLeuIeeHheSerLeuGlyArgHisThrAr 206
                                                                GCAGTTCCTGTTCGCGGAATTTTCT........
                                                                                                         gGlnMetArgAsnThrValAlaGlySerArgValProGlyArgGlyAlaP 223
                                                                                                                                                       GTGCAGCTGCTGCTCCTCGAGGAATTTTCTCTCTGGTTCCTGACTGC 6767
                                                                                                                                                                                                                                                GGCGCAGCTGCTCCTCCTGCAGGAATTTTCTCTGCCGTTGCTGCCG 6817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLy 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LysMetAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIl 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGGAATTTTCTGTCGCGGTCGTGACG.....CAGCTGTTGTTCGCGCCTC 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hrAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
2512..8070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49.458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106.00
0.774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 23.827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 9551
                                                                   6742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39
```

```
; NAME/KEY: CDS;
; LOCATION: 959..184
; OTHER INFORMATION:
US-08-137-175A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /cgn2_6/ptodata/2/ina/5A_comB.seq:US-08-137-175A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patent No. 5777095
                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6741
                                                                      FEATURE:
                                                                                                                                       FEATURE:
                                                                                                                                                                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US92/08972
FILING DATE: 22-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, Iver P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6643 GTTCCTCTTCGCGGAATTTTCTGTGACGCTC 6613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6693 GTCACGCTCTTGGCGGTGCAGCTGCTGTTCTTCCCTTTCCTGGAGCAGCT 6644
                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HANSSON, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          256 gPheIlePheLeuPhePheIleLeuValIle 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                  OTHER INFORMATION:
                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                  ORGANISM: Borrelia burgdorferi
STRAIN: Ip90
                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/OFFILING DATE: 26-OCT-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 419 Seventh Street, N.W., CITY: Washington STATE: D.C.
                                                                                                                                                   INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HisCysMetIleLysValPheLeuSerSerLeuLysPheHisIleArgAr 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..GTCACGCTCTTGGCGGCGCAGCTGTTGTTCCTCCTCCAGGAATTTTCT 6694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20004
                                                                                                                                                                                                                                                                                                       1958 base pairs
                              CDS
959..1843
                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HANSSON, Lennart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BARBOUR, Alan G.
BERGSTROEM, Sven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BROWDY AND NEIMARK
                                                                                                                                                                                                                                      CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                   .949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPROVEMENT IN BORRELIA BURGDORFERI AND PROPHYLAXIS
              /product= "OspB'
                                                                                 /product= "OspA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/137,175A
                                                                                                                                                 Isolate from I. persulcatus from Soviet Union
                                                                                                                                                                                                                                                                                                                                                                                                                                           28,005
                                                                                                                                                                                                                                                                                                                                                                                                                            BARBOUR-1B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300
```

alignment_scores

203 rgHisThrArgGlnMetArgAsnThrValAlaGlySerArgValProGly 219	CTTTG	GlyPh :::: AAGT	120 MetArgIleSerLysLeuValProTrpMetIleLeuGlySerLeuLeu 135 ::::::::::::::::::::::::::::::::::::	rValArgHisProLeuPheIle ::: CCTTCTGTAACTTTTAATGTTC	LeuTrpLeuAlaThrTrpLeuGlyValPheT IGT	70 IlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaIleLeuLe 86 767 CAGTTTTTTAGTAGCCTGAGTAGTGTCAGAGTCATTAAGCTCAACTGTT 718	64 yrvalasnValIleVal 69 :: 817 TCGGCTATTCACACTAATTGTTAAAGTGGAAGTCTTTGAATCCCATGTTC 768	CTTT	euLeuS	TTCTTTAAGCGTTGT	nGlyIleIleValVa	1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIle 15 ::: ::: :::::::::::: ::: 1034 GTTTTGGCTCAGCACCTTTTTGTCCACATGCTATTAAAGCTAATACTAAA 985	lign seg 1/1 to reverse of: US:	lignment_block: US-09-510-332-1 x US-08-137-175A-7/rev	Quality: 104.50 Length: 349 Ratio: 0.611 Gaps: 21 Percent Similarity: 48.997 Percent Identity: 23.496
	165 hrileGinLysGluAspThrLeuAlaileGinIlePheSerPheValAla 18 ::::::::::::::::::::::::::::::::::::	152 lproTyrPheLeuArgLysPhePheSerGlnAsnAla	136 TyrvalSerMetileCysValPheHisSerLysTyrAlaGlyPheMetva 15 ::::::::::::::::::::::::::::::::::::	120 MetargileSerLysLeuValProTrpMetIleLeuGlySerLeuLeu 13 ::::::::::::::::::::::::::::::::::::	103 yrCysalalysValalaSerValArgHisProLeuPheIleTrpLeuLys 1.	86 uphelleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheT 10: ::::::::::::::::::::::::::::::::	70	64 yr	56 ePheLeuGlnLeuPheIlePheT 64	40 LysMetAlaProLeuAspLeuLeuCeuSerCysLeuAlaValSerArgI1 56 ::::::::::::::::::::::::::::::::::::	32 lylleAspLeulleLysHis	16 .GlnPheLeuLeuGlyIlePheThrAsnGlyIleIleValValAsnG 32 ::: ::: ::: :::	1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIle	ign seg 1/1 to reverse of: US-08-137-175A-7 from: 1 to: 195 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIle	ignment_block: S-09-510-332-1 x US-08-137-175A-7/rev S-09-510-332-1 x US-08-137-175A-7 from: 1 to: 195 1 MetheudluserHisteutleitgyrPhetheuteuAlaVallie
189IlepheLeuPheAlaValLeuLeuIlepheSerLeuGlyA 203	165 hrileGinLysGluAspThrLeuAlaIleGinIlePheSerPheValAla 18 ::::::::::::::::::::::::::::::::::::	152 lproTyrPheLeuArgLysPhePheSerGlnAsnAla	136 TyrvalSerMetlleCysValPheHisSerLysTyrAlaGlyPheMetVa 15 ::::::::::::::::::::::::::::::::::::	120 MetargileSerLysLeuValProTrpMetIleLeuGlySerLeuLeu 13 ::::::::::::::::::::::::::::::::::::	103 yrCysAlaLysValAlaSerValArgHisProLeuPheIleTrpLeuLys 11	86 uphelleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheT 10: ::::::::::::::::::::::::::::::::	70 IlephephelleGluPhelleMetCysSerAlaAsnCysAlaIleLeuLe 86	64 yr	56 ePheLeuGlnLeuPheIlePheT 64	40 LysMetAlaProLeuAspLeuLeuCeuCysLeuAlaValSerArgI1 56 :::::::	32 lylleAspLeuIleLysHis	16. GlnPheLeuLeuGlyllePheThrAsnGlylleIleValValAsnG 32	1 MetleuGluSerHiSleuIleIleTyrPheLeuLeuAlaValIle	1 MetLeugluserHisleuIleIIeyrPheLeuLeuAlavalIle	ignment_block: S-09-510-332-1 x US-08-137-175A-7/rev S-09-510-332-1 x US-08-137-175A-7/rev 1 MetLeuGluserHisLeuIletleTyrPheLeuLeuAlaValIte 15 1 MetLeuGluserHisLeuIletleTyrPheLeuLeuAlaValIte 15 1034 GTMTGGCTCAGACCTTTTTGTCCACATGCTATAAACCTAATA 985 16 .GInPheLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnG 32 11 ::: ::::::::: :::::::::::

PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/13 FILING DATE: 26-OCT-1993 APPLICATION NUMBER: PCT/US93 APPLICATION NUMBER: PCT/US93 APPLICATION NUMBER: PCT/US93 APPLICATION NUMBER: PCT/US93 APPLICATION NUMBER: 28.005 REGISTRATION NUMBER: 28.005 REFERENCE/DOCKET NUMBER: BAT TELECOMMUNICATION INFORMATION: TELEPHONE: 202-628-5197 TELEFAX: 202-737-3528 TELEX: 248633 INFORMATION FOR SED ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 1958 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA ORIGINAL SOURCE: ORGANISM: BOTTELIA burgdorf: STRAIN: 150LATE: Isolate INDIVIDUAL ISOLATE: Soviet	Seq_documentation_block: Sequence 7, Application US/08479017 Sequence 7, Application US/08479017 Patent No. 6143872 GENERAL INFORMATION: APPLICANT: BARBOUR, Alan G. APPLICANT: BERGSTROEM, Sven APPLICANT: HANSSON, Lennart TITLE OF INVENTION: IMPROVEMENT TITLE OF INVENTION: PROPHYLAXIS NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSEE: BROWDY AND NEIMARK STREET: 419 Seventh Street, N CITY: Washington CITY: Washington STATE: D.C. COUNTRY: USA IP: 2004 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DO SOFTWARE: Patentin Release #1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/479 FILING DATE: OFFICIATON.	220ArgGlyAlaProI :: : 339 CCGTTGTTTTATCAGAACTTCCTT 232 rPheLeuIle.LeuTyrPheSerHi ::::::! 289 CATTAGACTGTATTTAC
8/137,175 3 7US92/08972 2 5 BARBOUR-1B ION: 7: dorfer1 late from I. persulcatus from late from I. persulcatus from iet Union	Aan G. Sven DEWARK DEWINDERENT IN BORRELIA BURGDORFERI AND OPHYLAXIS 2 D NEIMARK Street, N.W., Suite 300	CCGTTGTTTTATCAGAAGTTCTTTTAAGCTCAAGCTTGTTGTTTATCAGAAGTTCCTTTAAGCTCAAGCTTGTTCTTTACTAGACTTGTTGC 290 rpheLeuile.LeuTyrpheSerHisCysMetileLysValpheLeuSer 248 :::::

```
FEATURE:
NAME/KEY: CDS
COCATION: 125..949
OTHER INFORMATION: /product- "Ospa"
FEATURE:
NAME/KEY: CDS
LOCATION: 959..1843
OTHER INFORMATION: /product- "Ospb"
US-08-479-017-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-510-332-1 x US-08-479-017-7/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: US-08-479-017-7 from: 1 to: 1958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 104.50
Ratio: 0.611
Percent Similarity: 48.997
165 hrIleGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAla 181
                                                                               550 TCCATTTGCTCTTACTATTGTTTTTTCAGATGCTTCACCCTTTGCGTTGA 501
                                                                                                           136 TyrvalSerMetIleCysValPheH1sSerLysTyrAlaGlyPheMetVa 152
                                                                                                                                                                                                                                             644 CAGCAGCTAGAGTTCCTTCAAGAGCCAAAGTCTTTTAAAAACTTCTTTAGCT 595
                                                                                                                                                                                                                                                                         120 MetArgIleSerLysLeuValProTrpMetIleLeu..GlySerLeuLeu 135
                                                                                                                                                                                                                                                                                                                             694 TTTGCTTAAAACAACAGTGCCTTCTGTAACTTTTAATGTTGTTTTTGCCGT 645
                                                                                                                                                                                                                                                                                                                                                    103 yrCysAlaLysValAlaSerValArgHisProLeuPheIleTrpLeuLys 119
                                                                                                                                                                                                                                                                                                                                                                                                      767 CAGTTTTTTTAGTAGCCTGAGTAGTGTCAGAGTCATTAAGCTCAACTGTT 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       817 TCGGCTATTCACACTAATTGTTAAAGTGGAAGTCTTTGAATCCCATGTTC 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    867 TTTTGTACTGTTATTGTGTCTTCTTTTGTGAATACAAGGTTTTTGGTTTT 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     905 CTGCTTTGCCTTCTAGATTGG......TGCCTG...CTGAGTCGTAT 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             955 CTCTCCCTATTTTAAAGCATCTTTAAGTTCTTTAAGCGTTGTAATTTCGA 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 uPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 IlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaIleLeuLe 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 yr.....ValAsnValIleVal 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 ePhe.....LeuGlnLeuPheIlePheT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40 LysMetAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIl 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 lyIleAspLeuIleLysHis......Arg 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 .GlnPheLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnG 32
                                                                                                                                                              TTT...CCGGTTTTATCGCTTTTTATGTCTGTGTATTCAAGT...CTGGT 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 349
Gaps: 21
Percent Identity: 23.496
```

		RISTICS: base pairs	•• ••
		235-0176	
		INFORMATION:	٠. ٠.
•		<u> </u>	٠. ٠.
		NAME: Israelsen, Ned	
		10-SEP-199 ON: 435	
		?: US/	
		In Release # DATA:	٠. ٠.
		SYSTEM: PC-DOS/MS-DOS	•••
		MEDIUM TYPE: Floppy disk	٠. ٠.
		ER READABL	٠. ٠
		93660 St: US	
		STATE: California	•• •
		20 Newpo	٠
		PONDENCE ADDRESS:	
ING PROTEINS	E BINDING	ENCES: 45	٠
		E OF INVENTION: BINDING DOMAINS FRO	
		APPLICANT: Wellems, Thomas E.	
		ICANT: Peterson, Davi	. . .
		ICANT: Miller, I	•••
			٠.
		ENERAL INFOR	 G
		docum	seq ;
		_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-487-826B-13	seq_
		CCCAATAAATATTTT	
		uIleLeuIle	
	6	195 AGGCTGCTAACATTTTGCTTACATGCTATTAATGCTAATATTAGACCTAT 146	
	9	26	
	ŏ	A 19	
	9	SerLeuLysPheHisIleArgArgPheIlePhe 25	
	6	TTTTCTTTACTTACAA 24	
	8	32 rPheLeuIle.LeuTyrPheSerHisCysMetIleLysValPheLeuSer 24	
	ŏ	339 CCGTTGTTTTTATCAGAAGTTCCTTTAAGCTCAAGCTTGTCTACTGTTGC 290	
	ລັ	220ArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSe 232	
	0	റ-	
	19	203 rgHisThrArgGlnMetArgAsnThrValAlaGlySerArgValProGly 219	
	8	ω S	
)3	189IlePheLeuPheAlaValLeuLeuIlePheSerLeuGlyA 203	
	1	TGTTTTGCCATCTTCTTTGAAGATTTCAAATGTGGTT	
	38	182 Gluphe188	

```
alignment_block:
US-09-510-332-1 x US-08-487-826B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-487-826B-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-08-487-826B-13 from: 1 to: 19124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17696 TGTTTTTGGTATATTTGTAAAAAATATGTTTTTTTTTATAATCATATTAT 17745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17546 TGTTAATAATAAAAAGGAGATTTTCGAAGAGGAATATCCTATATCAGATA 17595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17496 ACTAATAATAATATGGATGTACCTACTAAAATGCACATCGAAATGAATAT 17545
                                                                                                                                                                                                                                                                                                                                                                                                                     17925
                                                                                                                        17960 CTAATATATATATCCTTCTATTTTCGATTTTTTCATTTTTTCCAGTATT 18009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CI
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                    18010
                                                                                                                                                               174
                                                                                                                                                                                                                                     157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 spLeuIleLysHisArgLysMetAlaProLeuAspLeuLeuLeuSerCys 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17 eLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleA 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 uLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CysSer...AlaAsnCysAlaIleLeuLeuPheIle...AsnGluLeuGl 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuAlaValSerArgIle......PheLeu......GlnLeu.P 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hellePheTyrValAsnValIleValIlePhePheIleGluPheIleMet 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                    erValArgHisProLeuPheIleTrpLeuLysMetArgIleSerLysLeu 125
                                                                                                                                                                                                                               rgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThrLeuAla 173
                                                                                                                                                                                                                                                                        ValProTrpMetIleLeuGlySerLeuLeuTyrValSerMetIle..... 140
                                                                                                                                                           IleGlnIlePheSerPheValAlaGluPhe.....SerValProLeuLe 188
                                                                                                                                                                                                                                                                                                                                            .....TTTTATTTTTAGTATAATAATTGTATCTATATTTGATTAATAA 1787
                                                .CysValPheHisSerLysTyrAlaGlyPheMetValProTyrPheLeuA 157
                                                                                     uIlePheLeuPhe.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
               .AlaValLeuLeuIlePheSerLeuGlyArgHisThrArg 206
:: = =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104.00
::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vaps: 15
Percent Identity: 21.148
                                                                                                                                                                                                  ....ATATATATATATAATTCTCTTTTT 17959
                                                                                             192
```

```
seq_name: /cgn2_6/ptodata/2/ina/6_COMB.seq:US-08-748-506-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                             ; MOLECULE TYPE: US-08-748-506-9
                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08748506 Patent No. 6159707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18060 TITATATATGTGTTTTATATGTGTTTTATTTTT.....GTTACT 18100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18192 AATTAATATATATATATATATATTTCTTGTTATTTTTATAAATATAACT 18241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18101 CTAATTCTGAATAATCCGAGCGAAAAAAAAATATATATCTC......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18242 AATTTCTTATTTTAATTTAACTTTAATTCCTTTTTAATTTCTTAATTCTT. 18290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18143 . АТАТАЛАЛАТТАТТАТАЛАТАСАЛТАТАТАТАТАСТТТССТАТТАЛАЛТА 1819:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18339 АЛАЛЛАЛАЛАЛАЛАЛАЛАЛАТТАТТАТАТТАТАЛТАЛА 18377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                TELEFAX: 312-616-5700 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 Lysphe.HisIleArgArgPheIlePheLeuPhePheIleLeuValIleG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 GlnMetArgAsnThrValAlaGlySerArgValProGlyArgGlyAlaPr 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 LeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLys 296
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-007-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Ronnett et al. TITLE OF INVENTION: NOVEL SPERM RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60601-6780
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 312-616-5600
                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: Two Pr
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 08-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lylleTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnProLys 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....pheSerHisCysMetIleLysValPheLeuSerSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  olleSerAlaLeuLeuSerIleLeuSerPheLeuIleLeuTyr...... 237
                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                              LENGTH:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Leydig, Voit & Mayer, Ltd.
Two prudential Plaza, Suite 4900
                                                                                                                                                                                            984 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S
                                                                                                                                        linear
    103.50
0.690
                                                                                                                    DNA (genomic)
                                                                                                                                                           double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/748,506
                                                                                                                                                                                                                                        9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version
    Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #1
        265
12
```

```
seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-153-848-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-510-332-1 x US-08-748-506-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-748-506-9 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 56.604
                                                         754
                                                                                        246 PheLeuSerSerLeuLysPheHisIleArgArgPheIlePheLeu 260
                                                                                                                                                                                     229 erileLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysVal 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            132 lySerLeuLeuTyrValSerMetIleCysValPheHisSerLys..... 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 elleTrpLeuLysMetArgIleSerLysLeuValProTrpMetIleLeuG 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          373 TCCCTGGACCGCTTTCTGGCCATCTGCAAACCTCTACATTATCCAACCAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 Glyval...PheTyrCysAlaLysValAlaSerValArgHisProLeuPh 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323 TCGTCTATCTTGTCGTGGGGCCAACAGGTTTTTTCCTTTTGGCTGCGTTA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 273 TCTGTCAGGGAGGCAAAAGATTCCCTTTGGGGTCTGCTTCTCACAGGCCT 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 CCTCATGGGCAACATGCTCATAATTACCATCACCTGTGTGGAC..... 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83 laIleLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeu 99 ::: ||| :::: |||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69 lilePhe.......PheileGluPheileMetCysSerAlaAsnCysA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 ValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnValIleVa 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 yIlePheThrAsnGlyIleIleValValValAsnGlyIleAspLeuIleL 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 CACCTGAAGATCCTCTTCTTCCTACTGCACTTGCTGGCCTACTTGGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 HisLeu...IleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGl 20
                                             ATTGTCCTCTCTAATGTATGGCAGCTGTGCATTTATATACCTG 798
                                                                                                                                                                                                                                     lAlaGlySerArgValProGlyArgGlyAlaProIleSerAlaLeuLeuS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheSerp 179
                                                                                                                                                                                                                                                                                                                               ATAGCCATCTTTGCATACAGC.....AATATAGTAGT 686
                                                                                                                                                                                                                                                                                                                                                                               LeuLeuIlePheSerLeuGlyArgHisThrArgGlnMetArgAsnThrVa 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          heValAlaGluPheSerValProLeuLeuIlePheLeuPheAlaValLeu 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrAlaGly...PheMetValProTyrPheLeuArgLysPhePheSerGl 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCTTCCTCTCATGGCCAGTCCAGTT...GTGATGCTTTCCAAGACATTT 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATGAGCCCAAGGATGTGCTTCCTCGTTACTGTCTGTTTATTTTTGG 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTGGCAAATCTCTCCTGTTCAGAAACCAGGTCTATTGAGATGCTGTTT. 615
                                                                                                                                          .....TTTACCCTTGCTGTAATTGTGCTTTTTGCTTCCTTTCTT 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGAGTGTTGTTTATAACTACTGCTATCCCCCAGCTCCTCACCATCAT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 22.264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
```

```
alignment_block:
US-09-510-332-1 x US-08-153-848-39
                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-153-848-39
                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-153-848-39 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
; Sequence 39, Application US/08153848
; Patent No. 5759804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (312) 474-630
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                  383 GGCGCTCAGCTGATATCTTCATTGCTAGCCTGGCGGTG.......420
                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
APPLICATION NUMBER: US 07/977,452
ATTORNEY/AGENT IMPORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 31,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTED:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentID Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 1872 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                          41 etAlaProLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                       24 nGlyIleIleValValAsnGlyIleAspLeuIleLysHisArgLysM 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
58 LeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheIleG1 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF ENQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 6300 :
CITY: Chicago
STATE: Illino:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                  CGGTCTGGTGCTCTGGACC.....GTGTTTCGGAGCAGCCGGGAGAAGA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60606
                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
202..1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Godiska, Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                      103.00
0.678
43.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39:
                                                                                                                                                                                                                                                                                                                                                                               Length: 350
Gaps: 15
Percent Identity: 19.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31794
                                                                              57
```

271	261 1042 TG	252 he 992 AC	235 eL :: 963 GG	219 G1 931 CG	202 lyA: :: 887 CTG	185 lp. 	171 Thr ::: 787 GCC	154 yrP : 743 GCT	[42 LP] :: 593 CAT	26 Val 43 GTG	09 erva 	05 43 CGC	00 G1yV : 93 GGGA	91 euG 46 TGC	74 uPhe 21	20
TGACTTTGA	Phef	heHisIleArgArgPheIl :: ::: ACCACCTGGTGAAGACGCT	LeuTyrPhes ::: : GTGACCTTTG	GlyArgGlyAl CGCCGG	rgHisThr GCCACTTC	roLeuLeuIl ::: CCTTCACCAT	TGGGA	heLeuAr :::: ACATGG <i>i</i>	PheHisSerLys' ::: ATGGTGTTACGC	alProTrpMet TGGCCACGGC#	lArgHi GAGGCC	CAGCGTCTTC	alPheTyr :: ::: CCTTCTTC	euGluLeuTrpLe TGCCCCTGTGG	IleMetCy	
	heIleLeuVa :::::::: ;accrcrrccr	ArgPheIlePhe ::: ::::: AAGACGCTGTAC	liscysM TGTGCT	ese · · ·	ArgGlnMet. ::: CGCAAGGAA	ePheL ::: CATGC	.LeuAlaIleGlr :::::::: :GTGGGCCTTGG	ysPh	TyrAlac ::: ACCACCC	OTrpMetIleLeuGly ::: CACGGCAGTTCTTTGG	sProLeuPheI AGTGGCCAATG	TGCCTCAC	Cys GCAAGCTC	uAlaThrT : GCTACCT	SerAlaAs	
GlyHisSer	lileGly] :::::: CATGAAC	ePheLeu ::::::: :GTACATGCTG	etIleLysV GG	rAlaLeuLeuSe CTGCTCA	detArgAsnThr AACGC	euPheAlaValLeuLeu 	eGlnIlePheSerPheV : ::: : TGGGGTCTCGTCCACCA	ePheSerGlnAsnAlaThrI ::: ::: .TACTCCATGGTGGCCACTG	yPheMet. ::: GGACTTGG	SerLeuLe GTGCTGGC	uPheIleTrpLeuLysM :::: CAATGCTCGGCTGAGGC	CGGCCTCAG	AGCAGCTAC	rp :: ACACGTACC	nCysAlaIleLeuI GCTGACCTG <i>F</i>	:
LeuIleLeu	[leTyrPro. ::: \rCTTCCCCT	GGCAGCCI	alpheLeu	erIle CATC	nThrValAlaGly ::: ATCGAGGGC	euLeuLeuI ::::::: TCTTCATCG	rPheValAlaGi ::::: CACCACCGTGG	AlaThrIle ::: GCCACTGTG	 AGAACACC	uLeuTyrValSe ::: GGCCGCCCTCCT	letArg :: !TGCGG	CTTCGACC	CTCATCTT	GGGACTAT	eLeuLeuPheIle :: CCTGACCTTCGTO	
LeuIleLeuGlyAs	ACTGCACCT	GCTGCACTGG	SerSerLeuLy::::	LeuSerPheLe ::: ATCGTGGTGCT	ySerArgValP: 	lePheSe :: CCCAAAC	LuPhes GCTTTC	GlnLysGlu ::::: AGCTCAGAG	Valp CTAAGGTGC	SerMetIleCy: ::: CTGGCCATGCC	IleSerLy ::: GTCAGCGO	laLysValAl ::: :GCTACCTGGC	CGTCAACATG	ACTGGCCC	eAsnGl : : :GTGA	
AsnP	GCAT		CT Sp	uII :: GGT	8 8	ដ ∷ ស	SerVa 1	o o	rof 1	ysva 1 CTGT 6	6 ⊢	as 1 CA 5	TA:	11 4 11 4	luL 91 3GC 445	420
282	270 1091	260 1041	252 991	235 962	218 930	202 886	185 836	170 786	154 742	142 692	125 642	109 592	542	92	5 [õ

THIS PAGE BLANK (USPTO)

```
/ vgn2_/yggdata/geneseq/geneseqn/Na1998.DAT:V31718 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1998.DAT:V31718 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1999.DAT:V73805 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1997.DAT:T79064 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1997.DAT:T79064 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1997.DAT:T79066 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1997.DAT:T79065 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1997.DAT:T79065 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1999.DAT:T0947 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1999.DAT:T0947 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1999.DAT:T66496 + /cgn2_2/gcgdata/geneseq/geneseqn/Na1999.DAT:T07161 - /cgn2_2/gcgdata/geneseq/geneseq/geneseqn/Na1999.DAT:T07161 - /cgn2_2/gcgdata/geneseq/geneseqn/Na1999.DAT:T07161 - /cgn2_2/gcgdata/geneseq/geneseq/geneseqn/Na1999.DAT:T07161 - /cgn2_2/gcgdata/geneseq/geneseq/geneseqn/Na1999.DAT:T07161 - /cgn2_2/gcgdata/geneseq/geneseq/geneseq/Na1999.DAT:T07161 - /cgn2_2/gcgdata/geneseq/geneseq/geneseq/Na1999.DAT:T07161 - /cgn2_2/gcgdata/geneseq/geneseq/geneseq/Na1999.DAT:T07161 - /cgn2_2/gcgdata/geneseq/geneseq/geneseq/Na1999.DAT:T07161 - /cgn2_2/gcgdata/geneseq/geneseq/geneseq/Na1999.DAT:T07161 - /cgn2_2/gcgdata/geneseq/geneseq/geneseq/Na1999.DAT:T07161 - /cgn2_2/gcgdata/genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database: N_Geneseq_36:*
Database sequences: 480022
Database length: 187831343
Search time (sec): 75.850000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         search information blo
Query: US-09-510-332-1
Query length: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
                                                                                                                     /cgn2_2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cgn2_2/gcgdata/geneseq/geneseqn/NA1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_2/gcgdata/geneseq/geneseqn/NA1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -WODEL=frame+_p2n.model -DEV=xlp
-Q-/cgn2_1/USPTO_spool/US09510332/runat_06032001_093638_13668/app_query.fasta_1.359
-Q-/cgn2_1/USPTO_spool/US09510332/runat_06032001_093638_13668/app_query.fasta_1.359
-DB-N_Geneseq_36 -OFMT-fastap -SUFFIX=rng -GAPOP=12.000
-GAPEXT=4.000 -MINATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QAPOP=4.500 -QAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500
-GAPOP=6.000 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -START=1 -MATRIX=blosum62
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS-human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=PCt
-TRANS-human40.cdi -LIST=45 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -MINLEN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_2/gcgdata/geneseq/geneseqn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_2/gcgdata/geneseq/geneseqn/NA19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V21511
/cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T69547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -USER-US09510332_@CGN1_1_126 -NCPU-6 -ICPU-3 -LONGLOG -NO_XLPXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mar 15, 2001 1:49
2_/gcgdata/geneseq/geneseqn/Na1988.DAT:N81114 + 2_2/gcgdata/geneseq/geneseqn/Na1988.DAT:N8193 - 2_2/gcgdata/geneseq/geneseqn/Na1998.DAT:N60393 - 2_/gcgdata/geneseq/geneseqn/Na1997.DAT:N72813 - 2_2/gcgdata/geneseq/geneseqn/Na1997.DAT:X61605 + 2_2/gcgdata/geneseq/geneseqn/Na1999.DAT:X61605 + 2_2/gcgdata/geneseq/geneseqn/Na1999.DAT:X61605 + 2_2/gcgdata/geneseq/geneseqn/Na1999.DAT:X61605 + 2_2/gcgdata/geneseq/geneseqn/Na1999.DAT:X61605 - 2_2/gcgdata/geneseq/geneseq/geneseqn/Na1999.DAT:X61605 - 2_2/gcgdata/geneseq/geneseq/geneseqn/Na1999.DAT:X61605 - 2_2/gcgdata/geneseq/geneseq/geneseqn/Na1999.DAT:X61605 - 2_2/gcgdata/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/geneseq/gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-510-332-1 to: N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyright (c) 1993-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gcgdata/geneseq/geneseqn/NA1993.DAT:Q43543
                                                                                                                                                                                                                                                                         /gcgdata/geneseq/geneseqn/NA1996.DAT:705868
/gcgdata/geneseq/geneseqn/NA1995.DAT:887588
/gcgdata/geneseq/geneseqn/NA1995.DAT:844959
/gcgdata/geneseq/geneseqn/NA1999.DAT:844959
/gcgdata/geneseq/geneseqn/NA1997.DAT:974743
/gcgdata/geneseq/geneseqn/NA2000.DAT:251241
/gcgdata/geneseq/geneseqn/NA2000.DAT:251231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strd Orig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compugen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZSCORE ESCORE Le
NA1999.DAT:Z20861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
118
118
118
118
118
118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118
117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
120
120
                                                                                                                                                                                                                                                                                                                                                                                                                         117
117
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entation
515.72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153
157
164
166
156
169
168
                                                                                                                                                                                                                                                                                                                                                                                           170
182
181
                                                                                                                                                                                                                                                                                                                                 169
171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ).0126
).7707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .0242
.0244
.4982
                                                                                                                                                .6488
.1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .0702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .0440
.0444
.0702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1496
1841
3129
1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jacobs K,
Treacy M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-518580/43
DB; Y42388.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McCoy JM, L
Agostino MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US03458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= b
1189..1899
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2695
```

```
/cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:X20254
/cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:X80508
/cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:X23518
/cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:X52149
/cgn2_2/gcgdata/geneseq/geneseqn/NA1994.DAT:G62924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide sequence of the pt127_1 clone
The PNS and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, hematopoiesis regulating activity, tissue growth activity, hemostatic activity, activity, hemostatic activity, activity, hemostatic activity, activity, and tumor and thrombolytic activity, receptor/ligand activity, and tumor inhibition activity. The PNS are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or
                                                                                                                                                                                                                                                                         Claim 26; Page 113-114; 125pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                New polynucleotides encoding human secreted proteins used therapeutic, diagnostic and research purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:Z20861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98US-0075038
99US-0251600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; cDNA library; clone; transmembrane cloning; hybridization cloning; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1129..1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_except=
1150..1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lavallie ER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vallie ER, Collins-Racie LA,
Steininger RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pt127_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (pos:1318..1320,
                                                                                                                                                                                                                                                                                      d or transmembrane protein on acid sequence of the encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106.
106.
106.
106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Merberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134
156
127
143
143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                    hemostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.13
0.5999
27.43
3.29
3.54
```

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: 220861 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-510-332-1 x 220861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                           1615
                                                                                                                                                                                                                                                                                                                                            1573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1379 CTATTAATGCCTGGGCTGTAACCAACCATTTCAGCATCTGGGTTGCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1197 TAATGGCTTCATAGTGTTGGTAAATTCCATTGAGTGGGTCAAGAGACAAA 1246
                                                                                                                                                                                                                                                                                                                                                                                                                                      1247 AGATCTCCTTTGCTGACCAAATTCTCACTGCTCTGGCAGTCTCCAGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1147 ATCATTTTTCCATTCTAGTAGTGGTTACATTTGTTCTTGGGAATTTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function of bacteria, fungi, viruses and other parasites; effecting bodily characteristics such as, e.g. weight, color, skin, etc., effecting biorhythms or circadian cycles; enhancing fertility; treatment of depression; treatment of pain; hormonal or endocrine activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2695 BP; 858 A; 427 C; 486 G; 919 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 ysMetAlaProLeuAspLeuLeuSerCysLeuAlaValSerArgIle 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 rAsnGlyIleIleValValValAsnGlyIleAspLeuIleLysHisArgL 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 IleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheTh 23
TCTCAAGAAGATG.....
                                       {\tt sThrArgGlnMetArgAsnThrValAlaGlySerArgValProGlyArgG}
                                                                                                                                                                                                       hrLeuAlaIleGlnIlePheSerPheValAlaGluPheSerValProLeu 187
                                                                              ACTCTGTCCCTGTTATCTTTTCTGCTCTTAATCTGTTCTTTGTGTAAACA
                                                                                                                   LeuIlePheLeuPheAlaValLeuLeuIlePheSerLeuGlyArgHi
                                                                                                                                                                                                                                                                                                                             ATGGATGAGAGTATGTGGACAAAAGAATATGAAGGAAACGTG..... 1614
                                                                                                                                                               ACCTTTCAGATATGACTGTAACCACGCTTGCAAACTTA...ATACCCTTT
                                                                                                                                                                                                                                                                                     rPheLeuArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspT 171
                                                                                                                                                                                                                                                                                                                                                                                                              TGGGGTCTTTGTTATTT.....TTGGTTTGTCATCTTGTTGTGGTAAAC 1572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uPheIleTrpLeuLysMetArgIleSerLysLeuValProTrpMetIleL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGCAACTGTTTTGAATCCAGGTTCATATAGTTTAGGAGTAAGAATTACTA 1378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGTTTG.....CTCTGGGTAATATTATWACATTGGTA 1328
                                                                                                                                                                                                                                                                                                                                                                      .....ValPheHisSerLysTyrAlaGlyPheMetValProTy 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTTTCTTCACTTAAAAAGGAGAATTAAGAGTGTCATTCCAGTGATACTAT 1528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCCTCAGCATATTTATTTGCTCAAGATTGCCAATTTCTCCAACTTTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TrpLeuGlyValPheTyrCysAlaLysValAlaSerValArgHisProLe 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PheLeuGlnLeuPheIlePheTyrValAsnValIleValIlePhePheIl 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIle....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .....AsnGluLeuGluLeuTrpLeuAlaThr
                                                                                                                                                                                                                                                  ·····AGTTGGGAGATCAAATTGAGTGATCCGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         320.50
1.669
59.259
  Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324
11
29.938
                                                                                1742
                                                                                                                                                                                                                                                  1645
                                         221
                                                                                                                        204
                                                                                                                                                                 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1196
```

```
seq_documentation_block:
ID V62130 standard; DNA; 8952 BP
XX

AC V62130;

XX

DT 07-DEC-1998 (first entry)
XX

HSV-2 strain SB5; immunologic
KW HSV-2 strain SB5; imm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2007 GATTTTGTGTCAGATTAAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSV-2 strain SB5; immunological response induction; therapy; antiviral identification; viral protein inhibitor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSV-2 strain SB5 Contig ID 100 DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Herpes simplex virus type 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 heIleLeuVallleGly......IleTyrProSerGlyHis 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           290 sPheLeuLeuHisSerLysCys 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTGTCCTCATGCTCAGCCAAACTACTGCAATTATATACCCCTTCATTTCAT 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerLeuIleLeuIleLeuGlyAsnProLysLeuLysGlnAsnAlaLysLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysValPheLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GATCTCCAGATTCCAACACCAAGGTCCACATAAAAGCTTTGCAAACGGTG 1821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lyAlaPro......IleSerAlaLeuLeuSerIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uSerSerLeuLys.....PheHisIleArgArgPheIlePheLeuPheP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V62130
                                                                                                                                                                                                                                                                                                                                            /*tag= e
/product= "ORF#5 protein"
/product= "ORF#5 protein"
/product= "ORF#5 protein"
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= c
/product= "ORF#3 protein"
complement (4889..5407)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (5646..6650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "ORF#1 protein"
/transl_except= (pos: 1..2, aa: Ala-Xaa)
/note= "Xaa= unspecified amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers complement (1..1802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product= "ORF#4 protein"
                                                                                                                                                                                                                                                                                                                                        /product= "ORF#6 protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "ORF#2 protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247
```

(SMIK) SMITHKLINE BEECHAM CORP

```
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-510-332-1 x V62130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: V62130 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a Herpes simplex virus type-2 (HSV-2) DNA sequence of the invention. This sequence was isolated from HSV-2 strain SB5 (deposited as ATCC VR-2546), is designated Contig ID 100, and encodes 6 HSV-2 proteins. The proteins can be used for the treatment or prevention of disease, to induce an immunological response in a mammal or to identify inhibitors, activators or novel antivirals. Antagonists of the proteins can be used to inhibit a viral polypeptide. The DNA sequence or a vector containing it can also be used to induce an immunological
                                                                                                                                                                                                                                                                                                                                                                                                          8021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herpes simplex virus type-2 sequences – useful in, e.g. prevention and treatment of infection or inducing immunological response in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chan JY,
                                                                                                                                                                                                                                                                                                                 8071 TTCCTCTCTCTATC.....TA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8952 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 163-166; 748pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1998-286847/25.
P-PSDB; .W72001, W72002, W72003, W72004, W72005, W72006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Esser KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response in a mammal.
                                                                                                                                                                                                                                                                    103 rCysAlaLysValAlaSerValArgHisProLeuPheIleTrpLeuLysM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 yIlePheThrAsnGlyIleIleValValValAsnGlyIleAspLeuIleL 37
142 lPheHisSerLys...
                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 SerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTCTTCCTCTCT.....CTTTTCTTCTCCTCCTCCTATCCTCTTATC. 7982
                                                                                                                                                                                                                                                                                                                                                                                                            CTTTTTCTTTCTTCTTCTATTCTCTGCCTCTCTCCTTCTTACTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ysHisArgLysMetAlaProLeuAspLeuLeuLeuSerCysLeuAlaVal 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ephepheIleGluPheIleMetCysSerAlaAsnCysAla.IleLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerArgIlePheLeuGlnLeuPheIlePheTyrValAsnValIleValIl 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCATTCTTTCTCTACTC..... 8157
                                                                                                                                                                         etArgIleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyr 136
                                                                                                                                                                                                                         CTGT.....CACTCTATCTCTTTTCCCTTCTTTTATATGTGTCGTAT 8128
                                                                                                                                                                                                                                                                                                                                                            phelleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTy 103
                                             ValSer.....MetIleCysVa 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dabrowski-Amaral CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leary JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  126.50
0.878
44.037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1525 A; 3103 C; 2456 G; 1867 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent
  .....TyrAlaGlyPheMetValProT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Delvecchio AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 8952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ......CTGTTTCT 8020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       327
16
22.630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dillon SB;
                                                                                                                                                                                                                                                                                                                             8087
                                                                                                                                                                                                                                                                                                                                                                                                                      8070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
```

```
seq_documentation_block:
ID Q87587 standard; DN
                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1995.DAT:Q87587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8208 TCTCTCTTCCTTTTCCTTTAATATATTTTCTTTTACTCATCCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8258' TTTTCACTTTACTATTCCAT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8532 CTCTCTCCTCTGCTCACACTTACTTCCTCCTCCTCCCAATTTGTCTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 yrpheLeuArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAsp 170
                                                                                                                                                                                                                                                                                                                                                                                                                                             8582 CGTCTCTCACTCTTCTCCTTTCTCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 oGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSerPheLeuI 235
                                                                                                                                                                                                                                                                                    DNA encoding Leucocytozoan protozoa structural protein epitope
                                                                                                                                                                                                                                                                                                                  19-DEC-1995 (first entry)
                                                    (DOBU-) DOBUTSUYO SEIBUTSUGAKUTEKI SEIZAI KYOKAI. (NISS-) NISSEIKEN KK.
                                                                                                                             10-SEP-1993;
                                                                                                                                                          04-APR-1995
                                                                                                                                                                                     JР07089995-A.
                                                                                                                                                                                                               Leucocytozoan
                                                                                                                                                                                                                                           leucocytozoan protozoa; structural protein; epitope; vaccine; fowl; leucocytozoanosis; treatment; ss.
                            WPI; 1995-167252/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ThrLeuAlaIleGlnIlePheSer.....PheValAl 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aGluPheSerValProLeuLeu.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerArgValPr 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PheHisIleArgArgPheIlePheLeuPhePheIle.LeuValIleGlyI 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTCTC...ATATCTCACCTCTCGTTC......TCTCCCCTCT 8481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leLeuTyrPheSerHisCysMetIleLysValPheLeuSerSerLeuLys 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......IlePheLeuPheAlaValLeuLeuILePheSerLeu 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCACTTTCTCCCTCCTCCACTCTTCTCATCTTTTTTTCTCTACTCAACAT 8368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .........GTGTATCTCTCTCTCTTTTTTTCTCTCTCTTTATTTC 8318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       leTyrProSerGlyHisSerLeuIleLeuIleLeuGlyAsnProLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LysGlnAsnAlaLysLysPheLeuLeu 293
                                                                                                                                                                                                                  protozoa sp
                                                                                                  93JP-0226078
                                                                                                                              93JP-0226078
                                                                                                                                                                                                                                                                                                                                                                          DNA; 1686 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   8608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284
```

```
alignment_block:
US-09-510-332-1 x Q87587/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality: 125.00
Ratio: 0.801
Percent Similarity: 48.297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: Q87587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1363 CTTCTATCATTTCTTCAACTACTGGTGTTTCTTCTACTACTTCTTCA 1314
                                                                                                                                                                                                                                                                                                                                                                               1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1263 GACGACATCTTCTTCCACTACTGGTGTTTCTTCTATCATTTCTTCTTCAA 1214
172 LeuAlaIleGlnIlePheSerPheValAlaGluPheSerValProLeuLe
                                                                                                                                                                                                                                                                                                                 105 aLysValAlaSerValArgHisProLeuPheIle.TrpLeuLysMetArg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q87587-89 encode polypeptides having a whole or partial epitope of structural protein of Leucocytozoan protozoa (see R70491-93). The polypeptides and DNA encoding them are useful in the production of vaccines for the treatment of leucocytozoanosis of fowl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1686 BP; 915 A; 129 C; 382 G; 260 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 12-14; 20pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immune inducing polypeptide against Leucocytozoan protozoa in production of vaccines for treatment of leucocytozoanosis fowl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 IleIleTyrPheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheTh :::::: ||||||||||||
                                                                                                                            TTTTGTTCATTTGTTTTTCCTTGTACTTGTCCATTTTGTT.....
                                                                                                                                                                                                                                                 IleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValSe 138
                                                                                     heLeuArgLysPhePheSerGlnAsnAlaThrIleGlnLysGluAspThr 171
                                                                                                                                                                                                      ATTAGTTTTTTCTGTTTCTGTTCTTTTATTATCATATATCTTAATATTG 920
                                                                                                                                                                                                                                                                                                                                                                     TCGGATTTTGATTCA...TTAGTTACT...TTAATGTTATAATTTTGCTG 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTACAGGTGTTTCTATCATTTCTTCTTCAACTACAGGTGTTTCTTCT 116
                                                                                                                                                                    rMetIleCysValPheHisSerLysTyrAlaGlyPheMetValProTyrP 155
                                                                                                                                                                                                                                                                                                                                                                                                             AsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAl 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGTCCGGAATTCCGGCCTCTAGTAGCTTCATTTAATTCTGGTTTTTTCA 1064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCATTTCTTCAACTACTGGTGTTTCTTCAACAACTTCTTCAACTAC 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rAsnGlyIleIleValValValAsnGlyIleAspLeuIle.....LysH
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGATGAATTTTATTTTCATCTTCAAATATATTTGTAGTTGAATTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ile..GluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTACATTAGTTTCTTCTACTACATCTTCTTCCACTATTGGTGTTTCTTC 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....ValAsnValIleValIlePhePhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....AspLeuLeuSerCysLeuAlaValSerArgIlePhe.... 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .....LeuGlnLeuPheIlePheTyr......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 323
Gaps: 18
Percent Identity: 25.077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 1686
                                                 851
                                                                                                                                851
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful
```

```
seq_documentation_block:
ID T17115 standard; DNA; 3016 BF
XX
AC T17115;
XX
DT 06-JUL-1996 (first entry)
XX
Rhodopsin gene.
XX
KW Human; rhodopsin; transversio
KW probe; primer; hybridisation;
KW eye; rod; retina; diagnostic;
XX
FH Key
FT 5'UTR 202.294
FT 7 /*tag= c
FT 7 /*tag= c
FT 7 /*tag= g
FT 7 /*tag= g
FT 7 /*tag= g
FT 7 /*tag= g
FT 7 /*tag= h
FT 7 /*tag= h
FT 7 /*tag= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1996.DAT:T17115
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; rhodopsin; transversion; mutation; retinitis pigmentosa; probe; primer; hybridisation; polymerase chain reaction; PCR; eye; rod; retina; diagnostic; prenatal diagnosis; photoreceptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             563 ACTICITCITGITCIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 rLeuIleLeuIleLeu 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTTTTTCTTTTTTCTTCATCTTCATTTTTCAG.....CATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IlePheLeuPhePheIleLeuValIleGlyIleTyrProSerGlyHisSe 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCATCTTTTTCTTTTCAACATATATTTTTCATCTTCTTGTTCTTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leLysValPheLeu...SerSerLeuLysPheHisIleArg...ArgPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTTTTTCTAATTCTTTAAAATGTTCTTGTTCTTTTTTCTACATATACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....PheLeuIleLeu......TyrPheSerHisCysMetI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValProGlyArgGlyAlaProIleSerAlaLeuLeuSerIleLeuSer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erLeuGlyArgHisThrArgGlnMetArgAsnThrValAlaGlySerArg
|||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCTTTCTTATCATCTTTAT.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTTTACTTCTGATTTTTCTCATCTA.....TTTCTTCTGATTCTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....GTTCACTTCTACTTTTCTTCTAAAACT
                /*tag= g
/note= "Substitution with A in
362..381
                                                                                                                                                                                                                                                                                 /*tag= b
/note= "Alternative 5'-UTR"
complement (231..250)
                                                                               /note= "Binds probes T17119 (normal)"
                                                                                                                complement (355..369)
/*tag= f
                                                                                                                                                                                     /product= Rhodopsin complement (354..372)
                                                                                                                                                                                                                                   /*tag= c
/note= "Binds primer
295..5278
                                                                                                                                            Location/Qualifiers
200..294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                           348
                                                                                                                                                                                                                                                           (T17121)"
                                                                                             (mutant)
                                                                                                                                                            (mutant)
                              mutant sequence
                                                                                               and
                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            807
                                                                                               T17120
                                                                                                                                                             T17118
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds.
```

```
alignment_block:
US-09-510-332-1 x T17115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence encodes human rhodopsin, and is shown without introns. The full sequence, with introns, is shown in T17116. Substitution of histidine for the normal nonpolar amino acid proline at position 23, by substitution of C with A in codon-23, results in a dysfunctional or absent molecule, affecting rod function, and is linked with autosomal dominant retinitis playmentosa. Probes T17117 and T17119 bind to the C-to-A compared transversion mutation sequence, and probes T17118 and T17120 bind transversion mutation sequence. Primers 485 (T17122) and 502 to the corresponding normal sequence. Primers 485 (T17122) and 502 to the corresponding normal sequence. Primers 485 (T17121) to amplify mutant and normal sequences, respectively, by PCR. Mutations in the retinal degeneration slow protein and retinal rod coWP-phosphodiestorase genes are also implicated in retinitis planentosa. Detection of any of these mutations in a foetus or pagmentosa. Detection of any of these mutations in a foetus or
                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-MAR-1993;
24-JAN-1990;
11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Diagnosis of hereditary retinal degenerative diseases e.g. retinitis pigmentosa, - caused by a human photoreceptor protein mutation, by detection of the mutation by PCR amplification or hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5498521-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-159684/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berson EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3016 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Column 19-24; 71pp; English
                                                                                                                                                                                 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patient may be used in diagnosis.
                                                                                                                                                                                                                                                   409 ATGCTGGCCGCCTACATG.....TTTCTGCTGATCGTGCTGGGCTT
                                                                                                            484
                                                                                                                                                                                                                17 eLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleA 34
                                                                     50
                                                                                                                                                                                                                                                                                       1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh
                                  AACCTAGCGGTGGCTGACCTCTTCATGGTCCTAGGTGGCTTCACCAGCAC
\verb|nValIleValIlePhePheIleGluPheIleMetCysSerAlaAsnCysA|
                                                                   CysLeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAs
                                                                                                                                         spLeuIleLysHisArgLysMet...AlaProLeuAspLeuLeuLeuSer 49
                                                                                                                                                                                 CCCCATCAACTTCCTCACGCTCTACGTCACCGTC......
                                                                                                          .....CAGCACAAGAAGCTGCGCACGCCTCTCAACTACATCCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R93116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dryja TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-0033081.
90US-0469215.
91US-0805123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90US-0469215
                                                                                                                                                                                                                                                                                                                              T17115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                                       124.50
0.759
50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     689 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Binds primers 485 (T17122) (normal) and (mutant)" \label{eq:mutant}
                                                                                                                                                                                                                                                                                                                                  from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     863 C; 753 G; 711 T;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 328
Gaps: 16
Percent Identity: 20.732
                                                                                                                                                                                                                                                                                                                                  μ
                                                                                                                                                                                                                                                                                                                                  .
6
                                                                                                                                                                                                                                                                                                                                    3016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0 other;
                                                                                                                                                                                                                                                              449
                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   502
```

```
seq_documentation_block:
                                                                                                                                                                seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V21511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 CCTCTACACCTCTCTGCATGGATACTTCGTCTTCGGGCCCACAGGATGCA 625
                                                                                                                                                                                                            1234
                                                                                                                                                                                                                                                                                                                                                               1154
                                                                                                                                                                                                                                                                                                                                                                                                                                       1104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 laIleLeuLeuPheIle......AsnGluLeuGluLeuTrp...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          192
Staphylococcal bacteriocin BacRI
                                        17-AUG-1998
                                                                                                              V21511 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAACTTCCGCTTCGGGGAGAACCATGCCATCATGGGCGTTGCCTTCACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTTGGAGGGCTTCTTTGCCACCCTGGGCGGTGAAATTGCCCTGTGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aSerValArg......hisProLeu......PheIleT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGGTGGTCCTGGCCATCGAGCGGTACGTGGTGGTGTGTAAGCCCCATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTACACGCTCAAGCCGGAGGTCAACAACGAG.....TCTTTTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hePheSerGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGln 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rAlaGlyPheMetValProTyrPheLeuArg.....LysP 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LeuGlySerLeuLeuTyrValSerMetIleCysValPheHisSerLysTy 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rp.....LeuLysMetArgIleSerLysLeuValProTrpMetIle 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C....ATCCCCGAGGGCCTGCAGTGCTCGTGTGGAATCGACT 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCCAGGTA 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGTCATGGCGTGGCCTGCGCCGCACCCCCACTCGCCGGCTGG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eAlaValLeuLeuLeuIlePheSerLeuGlyArgHisThrArgGlnMetA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IlePheSerPheValAlaGluPheSerValProLeuLeuIlePheLeuPh 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....LeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAl 108
                                                                                                                                                                                                                                                                                                                     GlyHisSerLeuIleLeuIleLeuGlyAsnProLysLeuLysGlnAsnAl 288
                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTGGCATTCTACATCTTCACCCACCAGGGCTCCAACTTCGGTCCCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tIleLysValPheLeuSerSerLeuLysPheHisIleArgArgPheIleP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCATCATCATGGTCATCGCTTTCCTGATCTGCTGGGTGCCCTACGCCAG 1103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaLeuLeuSerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMe 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAGTCA...GCCACCACACAGAAGGCAGAGAAGGAGGTCACCCGGATG 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rgAsnThrValAlaGlySerArgValProGlyArgGlyAlaProIleSer 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTATGGGCAGCTCGTCTTCACCGTCAAGGAGGCCGCTGCCCAGCAGC 1006
                                                                                                                                                                                                                                                                                                                                                             TCATGACCATCCCAGCGTTCTTTGCCAAGAGCGCCGCCATCTAC..... 1197
                                                                                                                                                                                                                                                                                                                                                                                                 heLeu.....PhePheIleLeuValIleGlyIleTyrProSer
                                                                                                                                                                                                                                      aLysLysPheLeuLeuHisSerLysCysCysGln
                                                                                                                                                                                                                                                                                    .CGGAACTGCATGCTCACCATCTGCTGCCGC
                                      (first entry)
                                                                                                                                                                                                                                                      299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          956
                                                                                                                                                                                                                                                                                               1233
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1153
```

```
alignment_block:
                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                            US-09-510-332-1 x V21511/rev
                                                                                                                                                                            Align seg 1/1 to reverse of: v21511
                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                         staphylococcus aureus UT0007. The sequence of the BacRI operon of was determined by N-terminal sequencing of purified BacRI operon (see W54171), with back-translation and plasmid analysis. The BacRI operon includes the BacRI gene (see V21510), a homologue of the CylM gene of the cytolysin operon of Enterococcus faecalis whose function is involved in the maturation of pre-cytolysin, and ATP-transporter gene, biol and bio2 genes related to lactococcin biosynthesis and modification, and a gene involved in immunity function. BacRI peptides can be produced by construction of an expression vector containing an oligonucleotide or operon coding for BacRI, and use of the vector to transform host cells for BacRI expression. The entire BacRI operon has been cloned into coding for BacRI, and use of the vector has been cloned into the medium. BacRI is estive against many Gram-positive and Gram-negative organisms such as Bordetella bronchoseptica, Pasteurella multocida and call showing the substitution of the serioconfunctivitis, is especially sensitive. BacRI can also be used as an anti-cancer agent:
                                                                                                    Sequence 6755 BP; 3903 A; 1252 C; 1600 G;
79 erAlaAsnCysAlaIleLeuLeu.....PheIleAsnGluLeuGluLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Therapeutic proteinaceous substances from Staphylococcus aureus - useful to inhibit growth of wide range of prokaryotic or eukaryotic cells, e.g. Moraxella bovis causing infectious bovine keratoconjunctivitis
                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This polynucleotide comprises the bacteriocin BackI operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crupper SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-230316/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UNIV ) UNIV KANSAS STATE RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-SEP-1997;
19-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9812319-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BacRI; bacteriocin; antimicrobial; antibacterial; antibiotic; Moraxella bovis; infectious bovine keratoconjunctivitis; cancer;
                                     CTTTGTTTTGGGGGTGTGTTTTTTTTTTTTTTCCGTCCTTTTCCGTCTGTT
                                                                    ePheTyrValAsnValIleValIlePhePheIleGluPheIleMetCysS 79
                                                                                                                               LeuSerCysLeuAlaValSerArgIlePheLeuGlnLeuPhe.....Il
                                                                                                                                                                                                                                                                                                                                                                                                as an anti-cancer agent.
                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Page 19-23; 38pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Iandolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-0931999.
96US-0710561.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-US16758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aureus
                                                                                                                                                                                                                                                               1.029
50.840
                                                                                                                                                                                                                                                                                                 124.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                strain UT0007 (ATCC 55800)
                                                                                                                                                                                                                                                               Percent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOUND
                                                                                                                                                                                                                                                         Gaps: 13
Identity: 26.471
                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                              0 U;
                                                                                                                                                                          .
6
                                                                                                                                                                            6755
                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                               other;
     93
                                     809
                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q.
```

```
ID XXX ACC XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID T69547 standard; DNA; 1496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T69547
                                                                                                            CDS
                                                                                                                                                                                                                                               Pheromone receptor; vomeronasal sensory neuron; social behaviour; maternal behaviour; reproductive behaviour; fertility; hormone secretion; ss.
                                                                                                                                                                                                   Rattus
                                                                                                                                                                                                                                                                                                                                                                    Rat pheromone receptor VN4 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                            26-AUG-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551 CCGTTTTGCGTTCCCTTTTTGGTCTTCTTGGCTTTGGTTTCTTTCTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GluPheSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTTCTG...CGGCTTGCGTTTCGCGTCGCTTTTTTTTCGCTGGTTTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lPheLeuSerSerLeuLysPheHisIleArgArgPhe...IlePheLeuP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGTCTTCTGTGTTGTCTTCTTTTTTTTTTTTCT.....TTGCGCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hrIleGlnLysGluAspThrLeuAlaIleGlnIlePheSerPheValAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ePheSerLeuGlyArgHisThrArgGlnMetArgAsnThrVal...AlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGTG.......GTTGGCTTTTGCTTTTTCTTTTCTGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGGCTTCTTC......TTTTTTGTTCTTTTTTTTTTCGTTGGTGCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HisSerLysTyrAlaGlyPheMetValProTyrPhe......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lArgHisProLeuPheIleTrpLeuLysMetArgIleSerLysLeuValP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSerVa
:::|||:::
:::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..TGGGCCGTTTTG...TCCGTTTTGTTTGCTTCGTTTTTCTTGCGCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    roTrpMetIleLeuGlySerLeuLeuTyrValSerMetIleCysValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....LeuArgLysPhePheSerGlnAsnAlaT 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gp
                                                                       /*tag=
                                                                                                         Location/Qualifiers 351..1283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
```

WO9714790-A1

```
alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-510-332-1 x T69547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c cDNA clones (T69546-50) respectively code for rat pheromone receptors VN3, VN4, VN5, VN6 and VN7 (WJ9104-08), members of a covel family of presumed 7-transmembrane domain receptors that are covolutionary independent of the odorant receptors of the main colfactory epithelium. These clones, and a clone for VN2 (sequence not provided), were isolated from rat vomeronasal organ cDNA (libraries by PCR and hybridisation. A differential cloning method was used to isolate vN7 cDNA (T69545). VN1-VN7 (not VN2) clones have been deposited in pBluescript as ATCC 97294-97299. A human homologue, HG25 (T69551), has also been isolated. VN polypeptides can be expressed in host-vector systems for use in identifying modulators for control of maternal, reproductive and social behaviour, to increase fertility, control hormone secretion and to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: T69547 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecule encoding vertebrate pheromone receptor useful to identify modulators for control of reproductive and social behaviour, fertility and hormone secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-245107/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Axel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-0CT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 10; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1496 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulate food uptake in humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                     417 GTTGGCATCTTAGCTAACAGTATCCTGTTTTTTGGTCACCTGTGCATGCT
                                                                                                                                                                                                                                                                               517
                                                                                                                                                                                                                                                                                                                                                          467
                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 LeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleAspLe :::||||||::: |||
                                                                                                                                                                                                                                                                                                               52 laValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnValIle
                                                                                                                                                                                                                                                                                                                                                                                           35 uIleLysHisArgLysMetAlaProLeuAspLeuLeuLeuSerCysLeuA 52
                                                                                                                                                                                                                                    ValIlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaIleLe
                                                                                                                                                                                                                                                                                                                                                        CCTTGGAGAGAACAAGCCTAAGCCCATTCATCTCTACATTGCATCCTTGT 516
                                           TGCTGAATGTCTTTTGGATGATCACTCTCAGTTCTAAAAAATCCTGTTTA
                                                                                                                                                                                                   GACATGTTTATTTCTCAGGGGATATGGGATTCTACCTCATGCCAGTCCCT
                                                                                                                                                                                                                                                                               CCCTAACACTAATGCTG...CTTATAACTATGGGACTCATAGCTGCT 563
pheIleTrpLeuLysMetArgIleSerLysLeuValProTrpMetIleLe 131
                                                                                                                      TATCTATTTGCACAGGCTTTCGAGGGGTTTTACCCTTAGTGCTGCCTGTC
                                                                                                                                                       uLeuPheIleAsnGluLeuGlu.....LeuTrpLeuAlaThrT
                                                                            rpLeuGlyValPheTyrCysAlaLysValAlaSerValArgHisProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W19105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dulac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95US-0005698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96WO-US16637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   122.50
0.738
54.785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          340 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 303
Gaps: 11
Percent Identity: 20.792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 G; 474 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 1496
                                                   713
                                                                                                                              663
                                                                                                                                                                    98
                                                                                                                                                                                                                                                85
```

```
DT XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID V53631 standard; cD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V53631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 uGlySerLeuLeuTyrValSerMetIleCysValPheHisSerLysTyrA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1260 TGTGCCAGA 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201
                                                                                                                                                                   cancer; anorexia; asthma; Parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hypertrophy; psychosis; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; dyskinssia; Huntingdon's disease; Gilles de la Tourette's syndrome; type transport of the control of the
                                                                                                                                                                                                                                                                                                                                                                                                HNFDY20; G-protein coupled receptor; human; infection; HIV; pain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human 7-transmembrane receptor HNFDY20 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1998 (first entry)
Key
                                                                         Homo sapiens
                                                                                                                                           therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          laGlyPheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAla 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTCAAAGTCATCTCCAGAGCAAAGGGCCACCGAGACCATCCTGCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuGlyArgHisThrArgGlnMetArgAsnThr.....valAl 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTTTTTTATCGGTCTCATGGCCCTGTCCAGTGGGTACCTGGTGGCTTTC 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..PheLeuPheAlaValLeu.....LeuLeuIlePheSer 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTGTTACTCCAGAACAAGCATGTTTTCCACAACAATTGCTGTCAGGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nIlePheSerPheValAlaGluPheSerValProLeuLeuIle.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCTCAGATAATTTTATGTATGTTACTAAGTCCTGTTCATTTCTACCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thr.....lleGlnLysGluAspThrLeuAlaIleGl 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGTGCCTTTCTT.....CTCCTCTGTGTTCTCTACATGTGTTTTA 789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            aGlySerArgValProGlyArgGlyAlaProIleSerAlaLeuLeuSerI 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGTCACCTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....ACAAAGTTTAAACATAACTCTCCCCATCACATCTC 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTCTGGAGACACAGGAAGCAGGCCCAGCATCTTCACAGCACCGGCCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGAAAAGCGTATGACTAAG....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lyAsnProLysLeuLysGlnAsnAlaLysLysPheLeuLeuHisSerLys 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATTGTGTCCCATAGCTATGCCACTGTCAGCTCTTTTGTGTTTTATTTTCA 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eLeuVallleGlyIleTyrProSerGlyHisSerLeuIleLeuIleLeuG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TACTCAAGGATGAAGTTCAAGGATGGGTCAACATTCTACTGTGTCCAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuSerSerLeuLysPheHisIleArgArgPheIlePheLeuPhePheIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGAGTTTCTTTGTGGTTCTCTACATTTTGGAAAATGTT.....GTCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysValPhe 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CysCysGln 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA; 1841 BP
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .....TTATCGATTATTGCTACCCCTAACTTG
                                                                                                                                                   SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .ATATTGAGGTCAGTG 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
```

```
alignment_block:
US-09-510-332-1 x V53631
                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This isolated polynucleotide codes for HNFDY20 (see W59924), a covel human 7-transmembrane G-protein coupled receptor. HNFDY20 CC novel human 7-transmembrane from cDNA libraries derived from CC mRNA in cells of human testis and human liver using expressed CC sequence tag analysis. The invention relates to HNFDY20 CC polypeptides and recombinant materials and methods for their CC production. It also provides methods for using such polypeptides CC and HNFDY20 polynucleotides for treatment of infections such as acceptable, indeed a provides methods for using such polypeptides CC infections, and conditions including pain, cancers, anorexia, bypertension, unitary retention, osteoporosis, angina pectoris, CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy, and psychotic and neurological disorders, including CC mxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias, such as Huntingdon's CC disease or Gilles de la Tourette's syndrome. Gene therapy using CC under-expression of the protein. The invention also relates to CC methods of identifying agonists and antagonists and for using CC unch compounds to treat conditions associated with HNFDY20 can be used to treat with HNFDY20 contended. CC with inappropriate HNFDY20 activity or levels are also provided.
                                                                                                                                                                                                                                               Align seg 1/1 to: V53631
                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1841 BP;
                                                     3
                                                                                                                 26 eIlevalvalAsnClyIleAspLeuIleLysH1sArgLysMetAlap 43
                                                                                                                                                                                                10 PheLeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 3; Page 2-4; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides and polypeptides encoding a novel human 7-transmembrane receptor - useful for diagnosing and treating e.g. cancer, osteoporosis and Parkinson's disease and infections caused by HIV-1 or -2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-482962/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bergsma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP866126-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-FEB-1998;
        ..GTGGACGTGCTCCTGCTCAACCTGACCGCCTCGGACCTGCTCCTGCTG 484
                                           roLeuAspLeuLeuSerCysLeuAlaValSerArgIlePheLeuGln 59
                                                                                  GCTGGCCCTGGTGGTCTTCGTGGGCAAGCTGCAGCGCCGCCCGGTGGCC.
                                                                                                                                                            TTCTCGGTGTACCTTCTCACTTTCCTGGTGGGGCTCCCCCTCAAC...CT
                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           짇
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fuetterer WS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0820521.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98EP-0301122
                                                                                                                                                                                                                                                                                                                                                                 122.50
0.833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125..1330
/*tag- a
                                                                                                                                                                                                                                                                                                                                                49.662
                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 A; 538 C; 593 G; 376 T; 0 other;
                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                  Length: 296
Gaps: 18
Percent Identity: 23.986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     мао ју,
                                                                                                                                                                                                                                             to: 1841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sathe GM;
                                                                                    436
```

```
EXEXEXEX B
                                                                                                                                                                               seq_documentation_block:
                                                                                                                                                                                                             seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1993.DAT:Q43543
                                                                                                                                                                                                                                                 1086 CCCTGAACTCCTGTGTCGACCCCTTTGTCTACTACTTC 1123
Human; rhodopsin; mutant; retinal degeneration; primer; probe
                                            Rhodopsin gene.
                                                                                  11-NOV-1993
                                                                                                                          Q43543;
                                                                                                                                                           Q43543 standard; cDNA; 3129
                                                                                                                                                                                                                                                                                        249 erLeuLysPheHisIleArgArgPheIlePheLeuPhe
                                                                                                                                                                                                                                                                                                                                                                                                               986
                                                                                                                                                                                                                                                                                                                                                                                                                                                   232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 HisSerLysTyrAlaGlyPheMetValProTyrPheLeuArgLysPhePh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           720 CTGCTCACTGCAGCGTGGTCTACGTCATAGAATTCTCAGGGGACATCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 ly......SerLeuLeuTyrValSerMetIleCys.....ValPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     626 CGCTTCCTGAGTGTGGCCCACCCCTG....TGGTACAAGACCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      106 LysValalaSerValargHisProLeuPheIleTrpLeuLysMetArg..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 535 CCTGCCCTTCATCCTCTGCCCACTCTCTGGA.....TTCATCTTCTTCA 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89 snGluLeuGluLeuTrpLeuAlaThrTrpLeuGlyValPheTyrCysAla 105
                                                                                                                                                                                                                                                                                                                                TATCTGCGGTGAAAGCCCCGGCGTGGAGGATCTACGTGACGCTTCTCAGCA 1085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alProGlyArgGlyAlaProIleSerAlaLeuLeu.....SerIleLeu
                                                                                                                                                                                                                                                                                                                                                                                                         AACTTCCTTGTCTGGGCTTTGGGCCCTACAACGTGTCCCATGTCGTGGGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                         SerPheLeuIleLeuTyr.....PheSerHis.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGGGGCAGCCACCGCCGGCAGAGGAGG.........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuLeuIlePheLeuPheAlaValLeuLeuLeuIlePheSerLeuGlyAr 203
                                                                                                                                                                                                                                                                                                                                                                  ....Cys.....MetIleLysValPheLeuSerS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9......HisThrArgGlnMetArgAsnThrValAlaGlySerArgV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGATCATCACCAGCTACTGCTACAGCCGCCTGGTGTGGATCCTCGGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCCTCCTGCCGTGCGGCTGGAGATGGCTGTGGTCCTTTTGTGGTCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               le......GlnIlePheSerPheValAlaGluPheSerValPro 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eSerGlnAsnAlaThrIleGln.....LysGluAspThrLeuAlaI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACAGCCAG.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....GTGGCGGGCTGTTGGCGGCCACGCTGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCACCAATGGGACCTGCTACCTGGAGTTCCGGAAGGACCAGCTAGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .....IleSerLysLeuValProTrpMetIleLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCACCATCTATCTC...ACCGCCCTCTTCCTGGCAGCTGTGAGCATTGAA 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eIleGluPheIleMetCysSerAlaAsnCysAlaIleLeuLeuPheIleA 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGTTCCTGCCTTTCCGCATGGTGGAGGCAGCCAATGGCATGCACTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeuPheIlePheTyrValAsnValIleValIle......pheph 72
                                                                                (first entry)
                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                            261
                                                                                                                                                                                                                                                                                                                                                                  249
                                                                                                                                                                                                                                                                                                                                                                                                         1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
                                                                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       719
```

```
alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-510-332-1 x Q43543
                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q43543 from: 1 to: 3129
                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key Location/Qualifiers prim_transcript 200..1341 cbs 295..1341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probe or primer contg. sequence of human retinal degeneration slow protein mutant - used to diagnose hereditary retinal degenerative diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence given represents the human rhodopsin cDNA. Mutant versions of this sequence encode proteins which cause retinal degeneration. These sequences may be identified using primers/ probes described in the invention (see also Q43545-48) and may be used to diagnose hereditary retinal degeneration. This sequence is the closest approximation to the gene sequence as the sequence given in the specification is not printed clearly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9312134-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hereditary; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1993-214088/26.
P-PSDB; R38483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berson EL, Dryja TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUN-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3129 BP; 694 A; 999 C; 654 G; 735 T; 47 other;
                                                                                                                                                                                                                 450 CCCCATCAACTTCCTCACGCTCTACGTCACCGTC......483
                                                                                                                                                     484 ......CAGCACAAGAAGCTGCGCACCCCTCTCAACTACATCCTGCTC 525
                                                                                                                                                                                                                                                                             409 ATGCTGGCCGACATG......TTTCTGCTGATCGTCCTGGGCTT
                            576 CCTCTACACCTCTCTGCATGGATACTTCGTCTTCGGGCCCACAGGATGCA 625
                                                                                         526 AACCTAGCCGTGGCTGACCTCTTCATGGTCCTAGGTGGCTTCACCAGCAC 575
                                                                                                                                                                        34 spLeuIleLysHisArgLysMet...AlaProLeuAspLeuLeuLeuSer 49
:::||||:::|||::: :::||||||:::
                                                                                                                                                                                                                                                   17
                                                                                                             50 CysLeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAs 66
                                                             66
83 laIleLeuLeuPheIle......AsnGluLeuGluLeuTrp...
                                                                                                                                                                                                                                                                                                             1 MetLeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPh 17
                                                                                                                                                                                                                                               eLeuLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleA 34
                                                          nValIleValIlePhePheIleGluPheIleMetCysSerAlaAsnCysA 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92WO-US10536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0805123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                           122.50
0.756
49.541
                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 327
Gaps: 16
Percent Identity: 21.101
```

X 2 2	Y DE	D X	AC X	ID	seq														
W PCR primer; KSHY; ORF74; Kaposi's sarcoma; diagnosis; treatment; W G protein-coupled receptor; ss. X	Kaposi's sarcoma associated herpesvirus ORF74.	T 11-SEP-1998 (first entry)	x C V31718;	eq_documentation_block: DV31718	eq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V31718	288 aLysLysPheLeuLeuHisSerLysCysCys 298 : ::: :: 1242 CATGCTCACCACCATCTGCTGC 1263	272 GlyHisSerLeuIleLeuIleLeuGlyAsnProLysLeuLySGlnAsnAl 288 :::::::: ::: :: 1204 GTCATCTATATCATGATGATCAGCTGTTCCGGAACTG 1241	27 12	242 tileLysValPheLeuSerSerLeuLysPheHisIleArgArgPheIleP 259 ::::::::::::::::::::::::::::::::::::	226 AlaLeuLeuSerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMe 242 :::::::::::::::::::::::::::::::::::	209 rgAsnThrValAlaGlySerArgValProGlyArgGlyAlaProIleSer 225 ::::::: ::::::::::::::::::::::::::	192 eAlaValLeuLeuLeuTlePheSerLeuGlyArgHisThrArgGlnMetA 209	176 IlePheSerPheValAlaGluPheSerValProLeuLeuIlePheLeuPh 192	159 hepheSerGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGln 175 :::::::: 866 ACTACACGCTCAAGCCCGAGGTCAACAACGAGTCTTTTGTC 906	147 ralaGlyPheMetValProTyrPheLeuArgLysP 159	131 LeuGlySerLeuLeuTyrValSerMetIleCysValPheHisSerLysTy 147	108 aSerValargHisProLeuPheILeT 117 ::::	95LeualaThTTrpLeuGlyValPheTyrCysAlaLysValAl 108	626 ATTIGGARGGCTTCTTTGCCACCCTGGGCGGTGAAATTGCCCTGTGGTCC 675

Kaposi's

```
alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-510-332-1 x V31718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOXCCCCCXX
                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: V31718 from:
470 GTGAGGTACCTCCTGGTGGCATATTCTACGCGTTCCTGGCCCAAG.....
                             110 ValArgHisProLeuPheIle.....TrpLeuLysMetAr 121
                                                        420 ACTATTTATATGTCTACTTGGATATCTTCAGTGTTGTGTGCGTCAGTCTA
                                                                                                              382
                                                                                                                                                                  338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of ORF74 of Kaposi's sarcoma herpesvirus (KSHV) which encodes a G protein-coupled receptor. It can be used in the diagnosis and treatment of KHSV infection.
                                                                                                                                                                                                              288 CGATAGATATACTGCTCCTGGGTATCTGCCTAAACTCGCTGTGTCTTAGC
                                                                                                                                                                                                                                                                250 CACCTACATT.....TTTTGCAAGCACCGATCGCGGCAGGAG
                                                                                                                                                                                                                                                                                                              Isolated Kaposi's sarcoma-associated herpesvirus proteins - comprising antigenic membrane protein, G protein coupled receptor and cyclin protein used to develop products for diagnosis and
                                                                                                                                                                                                                             11 LeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1202 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 50-51; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; W37976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-261008/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cesarman E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9815289-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                         ATATCTCTA....TTGGCAGAAGTGTTGATGTTTTTGTTTCCCCAATAT
                                                                               euTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSer 109
                                                                                                                                   eMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluL 93
                                                                                                                                                                                      LeuPheIlePheTyrValAsnValIleValIlePhePheIleGluPheIl 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sarcoma herpesvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knowles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0728603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-US18216
                                                                                                                                                                                                                                                                                                                                                                                                                                  120.50
0.867
52.852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 47..1075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 A; 279 C; 311 G; 354 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a
                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                      ب
                                                                                                                                                                                                                                                                                                                                                                      .
6
                                                                                                                                                                                                                                                                                                                                                                      1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                263
14
22.433
                                                        469
                                                                                                                                                            381
                                                                                                                                                                                                                337
                                                                                                                                                                                                                                                                                                                 249
```

```
seq_name:
Kaposi's sarcoma-associated herpes virus nucleic acid - d1:hydro:folate reductase and is useful for treatment, proor diagnosis of Kaposi's sarcoma
                                                                                                                                                                                                                                                                                                         Kaposi's sarcoma; acquired immune deficiency syndrome; AIDS; DHFR; Bcl-2; dihydrofolate reductase; LUR; long unique region; vaccine; prophylaxis; diagnosis; treatment; HHVB; capsid protein IV; tegument protein IV; glycoprotein; kaposin; cyclin D; immediate early protein; IEP; OX-2; v-adh; G-protein coupled receptor; FGARAT; ds.
                                                             WPI; 1999-069741/06
                                                                                            Bohenzky RA,
                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK.
                                                                                                                                                        29-NOV-1996;
                                                                                                                                                                                       29-NOV-1996;
                                                                                                                                                                                                                                                   US5849564-A.
                                                                                                                                                                                                                                                                             Kaposi's sarcoma-associated herpesvirus.
                                                                                                                                                                                                                                                                                                                                                                                                     KSHV LUR DNA (nucleotides 105,301-137,507).
                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V73805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244 LysValPheLeuSerSerLeuLysPheHisIleArgArg 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   787
                                                                                                                                                                                                                      15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                652 CATGACTGCAGACTGCGACTGCATGTCAGAACCGTGTCAGTTACTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      561 CATTGGTGCTGTCGGGGGATGCCTGTCGACACAGGAGCAGGGTGGTCGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTTCCTGTTACCCCTG......GCCCTCCTTATTCTGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACCACGTACTAAATCTACTGGACACTCTGCTAAGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .....GTGATTGCTGCTGGTGCTGCTGTTTTTGTGTTTTTGCCTTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                euLeuSerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGGTAAGGGGG.......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nThrValAlaGlySerArgValProGlyArgGlyAlaProIleSerAlaL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGCTCTCACCTGGTGTGGTGAGGAGGACAAAGCTGCAAGCCAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             luPheSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIle 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eGlnLysGluAsp...ThrLeuAlaIleGlnIlePheSerPheValAlaG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gIleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValS
::::: ::: |||::::: :::: ||| ::::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erMetIle.....CysValPheHisSerLysTyrAlaGly 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ....AAGCAGTCCCTCGGATGGGTACTGACATCCGCTGCACTGTTAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....CCGGTCAGCAAGCAGGCCATGTGTTATGAGAACGCGGGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_2/gcgdata/geneseq/geneseqn/NA1999.DAT:V73805
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                         Chang Y,
                                                                                                                                                        96US-0770379.
                                                                                                                                                                                       96US-0770379
                                                                                          Edelman IS,
                                                                                          Moore
                                                                                          PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          883
                                                                                          Russo
            prophylaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        610
                                encodes
```

X X X S S S S S S S S S S S S S S S X X X

24725

```
alignment_block:
us-09-510-332-1 x V73805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24274 CACCTACATT.....TTTTGCAAGCACCGATCGCGGGCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24362 ATATCTCTA.....TTGGCAGAAGTGTTGATGTTTTTGTTTCCCCAATAT 24405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence is a fragment of the Kaposi's sarcoma-associated herpesvirus (KSHV) LUR (long unique region). This fragment contains coding regions for ORF65 which encodes capsid protein IV, ORF66, ORF67 which encodes to the necodes a glycoprotein, ORF69, K12 which encodes kaposin, K13, ORF72 which encodes cyclin D, ORF73 which encodes immediate early protein (IEP), K14 which encodes OX-2 (v-adh), ORF74 which encodes G-protein coupled receptor, ORF75 which encodes tegument protein/FGGRAT, K15, KSHV is a new human the Herpesvirus (HHV8) believed to cause Kaposi's sarcoma (KS) which is the most common form of neoplasm occurring in persons with acquired immune deficiency syndrome (AIDS). The DHFR protein is useful for vaccination, prophylaxis, diagnosis and treatment of a subject with Kaposi's sarcoma and for detecting expression of a DNA virus associated with Kaposi's
                                                                              24635
                                                                                                                                                                                                                                                                                                                                                                                       24494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Column 155-182; 109pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32207 BP; 7229 A; 9156 C;
                                                                                                                                 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43
                             166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGATAGATATACTGCTCCTGGGTATCTGCCTAAACTCGCTGTGTCTTAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eValValValAsnGlyIleAspLeuIleLysHisArgLysMetAla...P 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LeuPheIlePheTyrValAsnValIleValIlePhePheIleGluPheIl 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePheLeuGln 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluL
eGlnLysGluAsp...ThrLeuAlaIleGlnIlePheSerPheValAlaG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    euTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSer 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCTCCACAGGCTTGTGCAGACTTGAAATTTTTTTT.....T 24443
                                                                                                                                                                               CATTGGTGCTGTCGGGGGATGCCTGTCGACACAGGAGCAGGGTGGTCGAC
                                                                                                                                                                                                                                   erMetIle.....
                                                                                                                                                                                                                                                                                 ....AAGCAGTCCCTCGGATGGGTACTGACATCCGCTGCACTGTTAATTG
                                                                                                                                                                                                                                                                                                                              gIleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValS
                                                                                                                                                                                                                                                                                                                                                                                       GTGAGGTACCTCCTGGTGGCATATTCTACGCGTTCCTGGCCCAAG....
                                                                                                                                                                                                                                                                                                                                                                                                                                     ValArgHisProLeuPheIle.....TrpLeuLysMetAr 121
                                                                                                                            PheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
6
                                                                                 CCGGTCAGCAAGCAGGCCATGTGTTATGAGAACGCGGGAAA 24675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V73805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120.50
0.867
52.852
                                                                                                                                                                                                                             .....CysValPheHisSerLysTyrAlaGly 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 263
Gaps: 14
Percent Identity: 22.433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 32207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8713 G; 7109 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24361
                                                                                                                                                                                                                                                                                                                                                                                               24538
                                                                                                                                         166
                                                                                                                                                                                                                                                                                                                                               138
                                                                                                                                                                                          24634
                                                                                                                                                                                                                                                                                           24584
```

```
seq_documentation_block:
ID V19941 standard; DNA;
XX
AC V19941;
XX
DT 03-AUG-1998 (first &
XX
DT 03-AUG-1998 (first &
XX
XX
KSHV long unique cod:
XX
KSHV: HHV8; human he:
KW KSHV: HHV8; human he:
KW interleukin-6; IL-6;
KW complement-binding p.
KW complement-binding p.
KW immediate early prot.
KW lymphoproliferative '
KW lymphoproliferative '
KW lymphoproliferative '
KW HIV immune status; a
XX
Kaposi's sarcoma-ass
XX
ZY
FT CDS /*ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1998.DAT:V19941
                                                                                                                                                                                                                                                                                                                        F1 F1 F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24676 CATGACTGCAGACTGCGACTGCATGTCAGAACCGTGTCAGTTACTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24761 TATGCTCTCACCTGGTGTGTGGTGAGGAGGACAAAGCTGCAAGCCAGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 luPheSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V19941 standard; DNA; 137507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis; complement-binding protein; glycoprotein; capsid protein IV; infection; immediate early protein; Kaposi's Sarcoma; protective vaccine; lymphoma; lymphoproliferative disease; leukaemia; splenomegaly; mycosis fungoides; HIV immune status; anti-inflammatory agent; therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSHV long unique coding region and terminal repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSHV: HHV8; human herpes virus 8; macrophage inflammatory protein II; interleukin-6; IL-6; interferon regulatory factor; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaposi's sarcoma-associated herpes virus.
                                                                                                                                                          CDS
                                                                                                                                                                                                                     CDS
                                      CDS
                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TACCACGTACTAAATCTACTGGACACTCTGCTAAGGCGA 24907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysValPheLeuSerSerLeuLysPheHisIleArgArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....GTGATTGTTGCTGTGGTGCTGCTGTTTTTTGTGTTTTTGCTTCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      euLeuSerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIle 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nThrValAlaGlySerArgValProGlyArgGlyAlaProIleSerAlaL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PheSerLeuGly......ArgHisThrArg...GlnMetArgAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTTTCCTGTTACCCCTG....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAGGTAAGGGGG......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8699..11236
                                                                                                                                                                                                                                                                                                                                           /product= macrophage inflammatory protein complement (27137..27424)
                                                                                                                                                                                                                                                                                                                                                                                                       complement (21548..21832)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= glycoprotein B
complement (17261..17875)
                                    89600..90541
                                                                                                                                                      /product glycoprotein M complement (69412..69915)
                                                                                                                                                                                                                /product= protein T1.1 complement (58976..60175)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                              /product= glycoprotein L
complement (88410..88910)
                                                                                                                                                                                                                                                                                 28661..29741
                                                                                                                                                                                                                                                                                                                                                                                                                               'product= interleukin 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product= complement-binding protein
                                                                                                                                                                                                                                                                                                      product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag=
/product= interferon regulatory factor
                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                *tag=
                                                                                                                                                                                                                                                                                                                            *tag= e
                                                            product=
                                                                                                                                                                                                                                                                                                      interferon regulatory factor l
                                                            interferon regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .....GCCCTCCTTATTCTGTTT
                                                                factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24868
```

```
This sequence represents the long unique region and terminal repeat of CC the Kaposi's sarcoma-associated herpes virus (KSHY). KSHV is also known as human herpes virus 8 (HHY8). This sequence contains the DNAs of the CC invention which encode KSHY polypeptides selected from: (a) viral CC (c) viral IRF 1; (d) complement-binding protein; glycoproteins B, M or L; CC (d) capsid protein IV encoded by ORF65; and (e) immediate early protein encoded by ORF73. Labelled probes for the nucleic acid, proteins encoded by 1t, and antibodies (Ab) specific for the proteins are useful for CC detecting HHV8, specifically for diagnosis of Kaposi's sarcoma, in body fluids or tissue samples. HHV8 infections can be tracted with antisense CC protein. Ab may be used for prophylaxis or treated with antisense CC while the protein can be used in protective vaccines. Ab may also be used to differentiate between lymphomas, and HHV8 may be implicated in many CC splenomegaly and mycosis fungoides. Cells and animals containing the nucleic acid are useful for drug screening. HHV8-derived peptides can be inhibited with methotrexate. These can also be used to determine CC used as targets for antiviral drugs, e.g. dihydrofolate reductase gene the immune status of a patient infected with HIV. HHV8 derived protein CC e.g. treating rheumatoid arthritis. This sequence is stated as containing containing the many reading rheumatoid arthritis. This sequence is stated as containing the containing the many and the containing 
Sequence 137507 BP; 32579 A; 37795 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding Kaposi's sarcoma associated herpes proteins - useful for, e.g. detecting levels of HHV8 in, and preparation of vaccines for treatment of, HIV patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-SEP-1996;
10-OCT-1996;
13-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2; Page 135-203; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bohenzky RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JUL-1996;
25-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9804576-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sdo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0708678.
96US-0728323.
96US-0747887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0686350.
96US-0687253.
96US-0688814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96US-0757669.
96US-0686243.
96US-0686349.
                                            frames.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-US13346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= glycoprotein x complement (93636..94127)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product - capsid protein IV complement (123808..127296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= interferon regulatory factor 4 complement (111931..112443)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= immediate early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edelman IS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Moore PS,
35758 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Russo.
```

alignment_scores:

Quality: Ratio:

Length: Gaps:

263 14

31375

Η.

0 other;

```
seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T79064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
                                                                                                                                                                                                                                                                            130111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-510-332-1 x V19941
                                                                                                                                                                                                                                                                                                                                                                       130061 TATGCTCTCACCTGGTGTGTGGTGAGGAGGACAAAGCTGCAAGCCAGGCG 130110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: V19941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129976 CATGACTGCAGACTGGCGACTGCATGTCAGAACCGTGTCAGTTACTGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129744 ACTATTTATATGTCTACTTGGATATCTTCAGTGTTGTGTGCGTCAGTCTA 129793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129662 ATATCTCTA.....TTGGCAGAAGTGTTGATGTTTTTGTTTCCCAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129574 CACCTACATT.....TTTTGCAAGCACCGATCGCGGGCAGGAG 129611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129612 CGATAGATATACTGCTCCTGGGTATCTGCCTAAACTCGCTGTGTCTTAGC 129661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129527 ATACTCTCTCTGATT...TTCCTCATAAATGTTCTTGGAAATGGATTGGT 129573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 eMetCysSerAlaAsnCysAlaIleLeuLeuPheIleAsnGluLeuGluL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 roLeuAspLeuLeuLeuSerCysLeuAlaValSerArgIlePheLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 eValValAsnGlyIleAspLeuIleLysHisArgLysMetAla...P
                                                                                                                                                                                                                                                        GAAGGTAAGGGGG.....
                                                                                                                                                                                                                                                                                                                                                                                                           PheSerLeuGly......ArgHisThrArg...GlnMetArgAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTTCCTGTTACCCCTG.....
                                                     TACCACGTACTAAATCTACTGGACACTCTGCTAAGGCGA 130207
                                                                                                     LysValPheLeuSerSerLeuLysPheHisIleArgArg
                                                                                                                                                           .....GTGATTGTTGCTGTGGTGCTGCTTTTTTGTGTTTTTGCTTCCCT 130168
                                                                                                                                                                                                           euLeuSerIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIle 243
                                                                                                                                                                                                                                                                                                                    nThrValAlaGlySerArgValProGlyArgGlyAlaProIleSerAlaL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               luPheSerValProLeuLeuIlePheLeuPheAlaValLeuLeuLeuIle 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eGlnLysGluAsp...ThrLeuAlaIleGlnIlePheSerPheValAlaG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATTGGTGCTGTCGGGGGATGCCTGTCGACACAGGAGCAGGGTGGTCGAC 129934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGAGGTACCTCCTGGTGGCATATTCTACGCGTTCCTGGCCCAAG....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erMetIle......CysValPheHisSerLysTyrAlaGly 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gIleSerLysLeuValProTrpMetIleLeuGlySerLeuLeuTyrValS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValArgHisProLeuPheIle.....TrpLeuLysMetAr 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PheMetValProTyrPheLeuArgLysPhePheSerGlnAsnAlaThrIl 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ....AAGCAGTCCCTCGGATGGGTACTGACATCCGCTGCACTGTTAATTG 129884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euTrpLeuAlaThrTrpLeuGlyValPheTyrCysAlaLysValAlaSer 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuPheIlePheTyrValAsnValIleValIlePhePheIleGluPheIl 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuLeuAlaValIleGlnPheLeuLeuGlyIlePheThrAsnGlyIleIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ........CCGGTCAGCAAGCAGGCCATGTGTTATGAGAACGCGGGAAA 129975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 22.433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCCTCCTTATTCTGTTT
                                                                                                                                                                                                                                                                                                                       227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27
```

```
alignment_block:
US-09-510-332-1 x T79064
                                                                                                                                                                          alignment_scores:
                                              Align seg 1/1 to: T79064
                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _documentation_block:
T79064 standard; cDNA to mRNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allele; Xenopus laevis; melatonin; receptor; untranslated region; PCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T79064;
                                                                                                                                                                                                                                                               Sequences T79063-66 represent novel allelic genes of the Xenopus laevis melatonin receptor MEL-IA. The sequences encode proteins which are 65 amino acids shorter than those described in the prior art. Also the last 2 C-terminal amino acids encoded by these sequences are different from the previously known proteins. This sequence is a short form of the novel receptor MEL-IAA also known as Mel 1-c(alpha). As compared to the long form (T79063), the difference occurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The nucleotide sequence was isolated from CDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence was isolated from control inhibit adenylyl cyclase, but both protein MEL-IAA has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular scape.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus melatonin receptor MEL-1Aa short form coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 28-29; 62pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jockers R, Marullo S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ADIR ) ADIR & CIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9704094-A1
                                                                                                                                                                                                                       Sequence 1147 BP; 317 A;
                                                                                                                                                                                                                                                       phosphodiesterase.
2 LeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1997-132635/12
                                                                                                                                                         Quality:
                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95FR-0008947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-FR01167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product- MEL-1Aa receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                             118.00
0.752
53.401
                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strosberg
                                                                                                                                                                                                                            234 C;
                                                                                                                              Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1147
                                                  ţo:
                                                                                                                                                                                                                            242 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
                                                   1147
                                                                                                                                                                                                                            354 T; 0 other;
                                                                                                                                294
12
19.388
                     18
```

```
141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 ValPheTyrCysAlaLysValAlaSerValArgHisProLeuPheIleTr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          llleValllePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCCTGAGGAACAAGAAGCTGCAGAATGCTGGAAATCTCTTTGTTGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     eulleLysHisArgLysMetAlaProLeu...AspLeuLeuLeuSerCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCTGGGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleAspL 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCACCTCTGCCCTGGCGGTGGTTCTTATATTCACCATTGTTGTGGATGT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATAGCTATTTTCCAGAATGGGTGGACGCTTGGAAATATCCATTGTCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTGTCTATTGCCGATCTGGTTGTTGCTGTGTATCCCTATCCGGTAATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              erPheValAlaGluPheSerValProLeuLeuIlePheLeuPheAlaVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TyrAlaGlyPheMetVal.....ProTyrPheLeuArgLysPhePheSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCTTGGCCTGACATGGATACTAACTATAATTGCAATCGTGCCAAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leLeuGlySerLeuLeuTyrValSerMetIleCysValPheHisSerLys 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCACAGCCTGAGATATGACAAGCTTTATAATCAAAGAAGCACCTGGTGCT 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pLeuLysMetArgIleSerLysLeuVal......ProTrpMetI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGTCTTCAACATAACAGCCATAGCTATCAACAGGTATTGCTACATCTG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGTGGCTTCCTGATGGGACTCAGCGTT.....ATTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LeuLeullePheSerLeuGlyArgHisThrArgGln.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCAG....ACAGTGAGTTCCTCATACACCATAACAGTAGTGGTGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTTGTTGGATCACTACAGTATGACCCCAGGATTTTTTCTTGCACATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTTTATAGTCCCTCTTAGTGTTGTGACATTCTGTTACTTA...AGAATA
                                                                                                                     TGTTTTAAGCTATTTCATGGCCTATTTTAACAGTTGTCTCAATGCTGTTA
                                                                                                                                                       rIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysValP 246
                                                                                                                                                                                                                                                                               TIGTACTTTTTGCAGTTTGCTGGGCCCCCTTAAACTTTATCGGCCTTGCT 795
                                                                                                                                                                                                                                                                                                                                                            AAAGTTGACACAAACAGACTTGAGAAATTTCTTGACCATGTTTGTGGTCT
                                          TATATGGTGTGCTAAATCAAAACTTCCGCAAG
                                                                             heLeuSerSerLeuLysPheHisIleArgArg
                                                                                                                                                                                                   GTGGCCATTAATCCGTTTCATGTGGCACCAAAGATTCCAGAATGGCTGTT
                                                                                                                                                                                                                                     val.....ProGlyArgGlyAlaPro...IleSerAlaLeuLeuSe
                                                                                                                                                                                                                                                                                                                .....GlySerArg
                                                                                                                                                                                                                                                                                                                                                                                                .....MetArgAsnThrValAla.....
                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGGTTTTAGTGATCCAAGTCAAACACAGAGTTAGACAAGACTTCAAGCA
/cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T79066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....AATATATTGGTCATT.....TTGTCTG
                                                                                 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                                                                                                                                                                                                               216
                                                                                                                                                                                                                                                                                                                                                                                                                                                   695
                                                                                                                                                                                                           845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504
                                                                                                                                                                                                                                                                                                                                                                                                           213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          207
                                                                                                                              895
```

seq_name:

seq_documentation_block

```
alignment_block:
US-09-510-332-1 x T79066
                                                                                                                                                                                                alignment_scores:
                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                       Sequences T79063-66 represent novel allelic genes of the Xenopus laevis melatonin receptor MEL-1A. The sequences encode proteins which are 65 amino acids shorter than those described in the prior art. This sequence is a short form of the novel receptor MEL-1Ab also known as compared to the short form (T79066), the difference occurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The MEL-1Ab sequences also differ from known MEL-1A receptor sequences by 6 amino acids. The nucleotide sequence was isolated from CDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence was isolated from Sequence encodes a protein which is a 7 transmembrane receptor intracellular CGMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiesterase, but unlike MEL-1Aa (T79063) cannot to
                                                               Align seg 1/1 to: T79066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 33-34; 62pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allele; Xenopus laevis; melatonin; receptor; untranslated region; PCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss.
                                                                                                                                                                                                                                                 Sequence 1147 BP; 313 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; W25927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jockers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ADIR, ) ADIR & CIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09704094-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus laevis
 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus melatonin receptor MEL-1Ab short form coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T79066 standard; cDNA to mRNA; 1147
                           2 LeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLe
CTCACCTCTGCCCTGGCGGTGGTTCTTATATTCACCATTGTTGTGGATGT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1997-132635/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marullo S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95FR-0008947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96WO-FR01167
                                                                                                                                                118.00
0.747
53.741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= melatonin receptor MEL-lab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strosberg
                                                                                                                                                                                                                                               246 C; 240 G;
                                                                                                                                                  Percent
                                                                 ç
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AD.
                                                                                                                                              Identity: 19.388
                                                                                                                                                                Length:
Gaps:
                                                                                                                                                                                                                                               348
                                                                                                                                                                                                                                             T; 0 other;
                              18
```

```
246 heLeuSerSerLeuLysPheHisIleArgArg 256
                                                                                      846 TGTGTTAAGCTATTTCATGGCCTATTTTAACAGCTGTCTCAATGCTGTCA
                                                                                                                                                                                 796
                                                                                                                                                                                                                         217
                                                                                                                                                                                                                                                                                                                                                                                                                                             646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 rGlnAsnAlaThrIleGlnLysGluAspThrLeuAlaIleGlnIlePheS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     101 ValPheTyrCysAlaLysValAlaSerValArgHisProLeuPheIleTr 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 CCTGGGC.....TGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     170 TCCTGAGGAACAAGAAGCTGCAGAATGCTGGAAATCTCTTTGTTGTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 LeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rIleLeuSerPheLeuIleLeuTyrPheSerH1sCysMetIleLysValP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       erPheValAlaGluPheSerValProLeuIlePheLeuPheAlaVal 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATAGCTATTTTCCAGAATGGGTGGACGCTTGGAAATATCCATTGTCAGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lIleValIlePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI 84
  TCTACGGTCTGCTAAATCAAAACTTCCGCAAG
                                                                                                                                                                          GTGGCCATTAACCCACTCCACGTGGCACCAAAGATTCCAGAGTGGTTGTT
                                                                                                                                                                                                                    Val......ProGlyArgGlyAlaPro...IleSerAlaLeuLeuSe 229
                                                                                                                                                                                                                                                                   TTGTACTTTTTGCCGTTTGCTGGGCACCCTTGAATTTTATCGGCCTTGCT 795
                                                                                                                                                                                                                                                                                                                                                     AAAGTTGACACCAACAGACTTGAGAAATTTCTTGACCATGTTTGTGGTCT 745
                                                                                                                                                                                                                                                                                                                                                                                                                                           TGGGTTTTAGTGATCCAAGTCAAACACAGAGTTAGACAAGACTTCAAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LeuLeuIlePheSerLeuGlyArgHisThrArgGln......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTTTATAGTCCCTCTTAGTGTTGTGACATTCTGCTACTTA...AGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTGTTGGATCACTACAGTATGACCCCAGGATTTTCTCTTGCACATTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TyralaGlyPheMetVal.....ProTyrPheLeuArgLysPhePheSe 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTTGGCCTGACATGGATACTAACCATAATTGCCATTGTGCCAAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          leLeuGlySerLeuLeuTyrValSerMetIleCysValPheHisSerLys 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCACAGCCTGAGATATGACAAGCTTTTTAATCAAAGAAGCACCTGGTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pLeuLysMetArgIleSerLysLeuVal......ProTrpMetI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCAGTCTTCAACATAACAGCCATAGCTATCAACAGGTATTGCTACATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCAGTGGCTTCCTGATGGGACTCAGCGTT.....ATTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGTCTATTGCCGATCTGGTTGTTGCTGTATCCCTATCCGGTAATTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               euIleLysHisArgLysMetAlaProLeu...AspLeuLeuLeuSerCys
                                                                                                                                                                                                                                                                                                        .....GlySerArg
                                                                                                                                                                                                                                                                                                                                                                                                 .......................MetArgAsnThrValAla........
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAG....ACCGTAAGTTCCTCATACACCATAACAGTAGTGGTAGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly
927
                                                                                                                                                                            845
                                                                                                                                                                                                                                                                                                                                                                                                 213
                                                                                                                                                                                                                                                                                                                                                                                                                                             695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269
```

CDNA

to mRNA; 1311

/cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T79063

```
alignment_block:
US-09-510-332-1 x T79063
                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                              Percent Similarity:
                                                                                                  Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allele; Xenopus laevis; melatonin; receptor; untranslated region; PCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; SS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus melatonin receptor MEL-1Aa long form coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T79063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 melatonin receptor MEL-1A. The sequences encode proteins which are 65 amino acids shorter than those described in the prior art. Also the last 2 C-terminal amino acids encoded by these sequences are different from the previously known proteins. This sequence is a long form of the novel receptor MEL-1Aa also known as Mel 1-c(alpha). As compared to the short form (779064), the difference occurs in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the sequences encode the same protein), which is thought to affect the half-life of the mRNA. The nucleotide sequence was isolated from CDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a protein which is a 7 transmembrane receptor involved in cellular signalling. MEL-1Aa has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular components of the proteins can modulate intracellular shows before a protein scan modulate intracellular show
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-132635/12.
P-PSDB; W25926.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jockers R, Marullo S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ADIR ) ADIR & CIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9704094-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 25-26; 62pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequences T79063-66 represent novel allelic genes of the Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1311 BP; 369 A; 259 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphodiesterase.
91 CTCACCTCTGCCCTGGCGGTGGTTCTTATATTCACCATTGTTGTGGATGT 140
                                             2 LeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLe 18
                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                        :
0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95FR-0008947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96WO-FR01167
                                                                                                        T79063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= MEL·lAa receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..1065
                                                                                                                                                                                                                                118.00
0.752
53.401
                                                                                                           from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strosberg AD;
                                                                                                                                                                                                                                   Percent Identity: 19.388
                                                                                                           ب
                                                                                                                                                                                                                                                                                                                                                                                           269
                                                                                                           :
6
                                                                                                                                                                                                                                                                                                                                                                                         G; 414 T; 0 other;
                                                                                                                                                                                                                                                                                   Length:
```

	246 heLeuSerSerLeuLysPheHisIleArgArg 256 :: :: ::: ::::: ::: 896 TATATGGTGTGCTAAATCAAAACTTCCGCAAG 927	
24 89	229 rIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysValP :::: :::: :::	
84 84	217 ValProGlyArgGlyAlaProIleSerAlaLeuLeuSe	
79	rgggcccccttaaactt	
74.	ArgAsoThrValAla	
699	ln	
194	PheLeuPheAlaVal ::: TACTTAAGAATA	
178 598	lnIlePheS ::: TGGTGGTGC	
161 554	147 TyralaGlyPheMetValProTyrPheLeuArgLysPhePheSe: :::::::	
146 504	i s	
130 154	MetI TGCT	A 1
117 404	о r	س ب
100 354	84 leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly	w
84 319	CysSerAlaAsnCysAlaI ::: ::: GGAAATATCCATTGTCAGA	N
69	51 LeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa 6 :::::::::::::::::::::::::::::::::	N
0 19	35 euIleLysHisArgLysMetAlaProLeuAspLeuLeuLeuSerCys 50 	Η
69	18 uLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleAspL 35	

seq_documentation_block:
ID T79065 standard; cDNA to mRNA; 1312 BP
XX

seq_name: /cgn2_2/gcgdata/geneseq/geneseqn/NA1997.DAT:T79065

```
alignment_block:
                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                   Sequences T79063-66 represent novel allelic genes of the Xenopus laevis melatonin receptor MEL-1A. The sequences encode proteins which are 65 cc amino acids shorter than those described in the prior art. This sequence is a long form of the novel receptor MEL-1Ab also known as Mel 1-c(beta). CC As compared to the short form (T79066), the difference occurs in the 3' cc untranslated region (both sequences encode the same protein), which is CC thought to affect the half-life of the mRNA. The MEL-1Ab sequences also CC differ from known MEL-1A receptor sequences by 6 amino acids. The CC uncleotide sequence was isolated from cDNA derived from Xenopus skin RNA cand amplified using the primers T79067-76. The nucleotide sequence cc encodes a protein which is a 7 transmembrane receptor involved in CC cellular signalling. MEL-1Ab has been shown to modulate intracellular CC coMF, sep. inhibiting its accumulation induced by an inhibitor of CC comparativity.
                                                                                                              Align seg 1/1 to: T79065
                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                               US-09-510-332-1 x T79065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
                                                                                                                                                                                                                                                                                                 Sequence 1312 BP;
                                                                                                                                                                                                                                                                                                                                 cyclase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 30-31; 62pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allele; Xenopus laevis; melatonin; receptor; untranslated region; PCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase; ss.
• 18
                                               91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1997-132635/12.
P-PSDB; W25927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jockers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ADIR ) ADIR & CIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-FEB-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9704094-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus melatonin receptor MEL-lab long form coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T79065
                                                                       2 LeuGluSerHisLeuIleIleTyrPheLeuLeuAlaValIleGlnPheLe 18
     uLeuGlyIlePheThrAsnGlyIleIleValValValAsnGlyIleAspL 35
                                       CTCACCTCTGCCCTGCCGGTGGTTCTTATATTCACCATTGTTGTGGATGT 140
                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marullo S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95FR-0008947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96WO-FR01167.
                                                                                                                                                                                              118.00
0.747
53.741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= melatonin receptor MEL-1Ab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..1065
                                                                                                                                                                                                                                                                                               365 A;
                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strosberg AD;
                                                                                                                                                                                                                                                                                               271 C;
                                                                                                                                                                                          Length: 294
Gaps: 12
Percent Identity: 19.388
                                                                                                            to: 1312
                                                                                                                                                                                                                                                                                              267 G;
                                                                                                                                                                                                                                                                                            409 T; 0 other;
```

46 heLeuSerSerLeuLysPheHisIleArgArg 256 :: ::: ::: :::: ::: 96 TCTACGGTCTGCTAAATCAAAACTTCCGCAAG 927	ໝ ຄ
229 rIleLeuSerPheLeuIleLeuTyrPheSerHisCysMetIleLysValP 246 ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :: ::: ::: ::: ::: ::	oo ν
217 ValProGlyArgGlyAlaProIleSerAlaLeuLeuSe 229	7
46 TTGTACT	7
96 AAAC	
95 LeuLeuLeuIlePheSerLeuGlyArgH1sThrArgGln	0 0 1
99	5 H
55	or \vdash
147 TyralaGlyPheMetValProTyrPheLeuArgLysPhePheSe 161 :::::: :: ::	en 🗀
130 leLeuGlySerLeuLeuTyrValSerMetIleCysValPheHisSerLys 146	
117 pLeuLysMetArgIleSerLysLeuValproTrpMetI 130 :::::: ::: ! ::: 405 CCACAGCCTGAGATATGACAAGCTTTTTAATCAAAGAAGCACCTGGTTCT 454	
laSerValArgH1 :::::::::: TAGCTATCAACAG	
84 leLeuLeuPheIleAsnGluLeuGluLeuTrpLeuAlaThrTrpLeuGly 100	
67 lIleValllePhePheIleGluPheIleMetCysSerAlaAsnCysAlaI 84 ::: ::: ::: ::: ::: ::: ::: ::: :::	
51 LeuAlaValSerArgIlePheLeuGlnLeuPheIlePheTyrValAsnVa 67 :::::::::::::::::::::::::::::::::	
etAlaProLeuAspI :: 	
:::! ::::::::::::::::::::::::::::::::	

84 24

22 79 21 74 21

Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 61, Appli Sequence 61, Appli Sequence 61, Appli Sequence 61, Appli Sequence 5, Appli Sequence 6, Appli

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued_Patents_AA:*

1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-510-332-1
1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    March 15, 2001, 11:39:04; Search time 65.02 Seconds
                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                                                                                                                                                                                                                       Query
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174772 seqs, 17957048 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gapop 10.0 , Gapext 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLESHLIIYFLLAVIQFLLG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
Length
DΒ
         US-08-118-270-56
PCT-US93-08528-56
US-08-390-000A-8
US-08-390-000A-8
US-08-390-000A-8
US-08-748-506-22
US-08-748-506-23
US-08-728-603-17
US-08-748-506-24
US-08-748-506-24
US-08-118-270-65
PCT-US93-08528-65
US-08-148-209A-4
US-08-148-209A-4
US-08-148-209A-4
US-08-148-209A-4
US-08-148-209A-4
US-08-148-209A-4
US-08-18-710-44
US-08-18-18-70-44
PCT-US93-08528-68
US-08-118-270-68
US-08-118-270-68
US-08-118-270-68
US-08-118-270-68
US-08-118-270-68
US-08-118-270-68
US-08-118-270-68
US-08-118-270-68
US-08-118-270-51
US-08-118-270-51
                                                                                                                                                                                                                                                                                                                                                                                           IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ....GNPKLKQNAKKFLLHSKCCQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (without alignments)
82.577 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174772
                                                                                                                                                                                   Sequence 56, Appl
Sequence 8, Appl:
Sequence 8, Appl:
Sequence 2, Appl:
Sequence 23, Appl:
Sequence 17, Appl:
Sequence 17, Appl:
Sequence 12, Appl:
Sequence 12, Appl:
Sequence 17, Appl:
Sequence 17, Appl:
Sequence 18, Appl:
Sequence 11, Appl:
Sequence 11, Appl:
Sequence 11, Appl:
Sequence 65, Appl:
Sequence 65, Appl:
Sequence 65, Appl:
Sequence 65, Appl:
                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                Sequence
Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                           Sequence
Sequence
                                                                                                                      Sequence
Sequence
                                       Sequence
                                                    Sequence
                                                                   Sequence
                                                                               Sequence
 44, Appli
9, Appli
40, Appl
40, Appl
40, Appl
40, Appl
44, Appl
44, Appl
68, Appl
5, Appli
51, Appli
51, Appli
55, Appli
51, Appli
51, Appli
                                                                                              STRANDEDNESS:
; TOPOLOGY: line
; MOLECULE TYPE: P
US-08-118-270-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-118-270-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 50; Patent No.
    δã
                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION NUMBER: US 07/943,236
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, KEVIN G.
NAME: TOWNSEND, KEVIN G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Murphy, Randall B.
APPLICANT: Schuster, David I.
APPLICANT: Schuster, David I.
TITLE OF INVENTION: RECEPTORS, AND COUNTIED OF INVENTION: RECEPTORS, AND COUNTIED OF INVENTION: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., SI
                               Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                    NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44443335433334444433354
                                                                                                                                                                                           TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 419 Seven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
    1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56, Application US/08118270
5. 5508384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.1%;
ilarity 21.1%;
Conservative 64
                                                                                                                          SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-476-000-5
US-08-4772-840-5
US-08-476-976-5
US-08-476-976-61
US-08-4772-840-61
US-08-4774-410-61
US-08-4774-410-61
US-08-0776-093A-6
US-08-0776-093A-6
US-08-076-093A-6
US-08-801-265-6
US-08-803-478-6
US-08-803-478-6
US-08-803-478-6
US-08-803-238-6
US-08-803-238-6
US-08-801-238-6
US-08-801-238-6
US-08-801-238-6
                               ; Score 123.5; DB 1;
; Pred. No. 4.3e-05;
64; Mismatches 121;
                                                                                                                                                                                                                                                                 MURPHY-2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F G-COUPLED PROTEIN
COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suite 300
                                     Indels 73;
                                                           Length
```

Result No.

Score

123.5 123.5 123.5 122.5 120.5 120.5 120.5 120.5 110.5 118.5 118.5 118.5 119.5 119.5 119.5 119.5 119.5 119.5 119.5

55555555555555577777777777

100.5 100.5 100 100 99.5 99

Gaps

17;

Minimum DB Maximum DB

seq seq

Database

Title: Perfect score:

Scoring table: Sequence: Run 욪

protein

ı

```
á
                                                                                                                     PCT-US93-08528-56
                                                                                                                                                                         TELEX: 202-,,
TELEX: 248633
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
FRIGHT: 309 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 문
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US93-08528-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ъ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                 Query Match
Best Local Similarity
                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 56, Application PC/TUS9308528 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                       NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 GHSLILILGNPKLKQNAKKFLLHSKCC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                             TELEPHONE: 202 - 737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205 QKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMRIPAFFAKSAAIY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 GENHAIMGVAFTWV-MALACAAPPIAGW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 ---HPL----FIWLKMRISKLVP----WMILGSLLYVSMICVFHSKYAGFMVPYFLR--- 157
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -NPVIYIIFNKQF----RNCMLQLICC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLWLAIERYVVVCKPMSNFRF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFIFYVNVIVIFFIEFIMCSANCAILLFINEL-----ELWLATWLGVFYCAKVASVR- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York University
VENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
VENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                           single
                                   8.1%; Score 123.5; DB 4
21.1%; Pred. No. 4.3e-05;
ative 64; Mismatches 121
                                                                                                                                                                                                                                                                                                                                                                                 US 07/943,236
                                                                                                                                                                                                                                                                                                      MURPHY-2 PCT
                                   Mismatches 121;
                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----SRY----IPEGLQCSC 149
                                  Indels
                                                              Length
                                                              309;
                               73; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50
                               17;
```

B Ş

Matches

Conservative

Indels 71;

Gaps

16;

```
US-08-390-000A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-390-000A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ğ. δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08390000A Patent No. 5985583
GENERAL INFORMATION:
                                                                                                                                                                          TELEFAX: 212 869-8864/
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 69:
                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0
FILING DATE: 17-FEB-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263. -NPVIYIIFNKQF----RNCMLQLICC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 GHSLILILGNPKLKQNAKKFLLHSKCC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 QKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMRIPAFFAKSAAIY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 GIDYYTLKPEVNNE---SFVIYMFVVHFTIPLIIF-FCYGQLVFTVKEAAAQQQES-ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 --KFFSQNATIQKEDTLAIQIFSFYAEFSYPLLIFLFAVLLLIFSLGRHTROMRNTYAGS 215
                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York .
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 LGGFTSTLYTSLHGYFYFGPTGCNLEGFFATLGGEIALWSLWLAIERYVVVCKPMSNFRF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 LFIFYVNVIVIFFIBFIMCSANCAILLFINEL-----ELWLATWLGVFYCAKVASVR- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENHAIMGVAFTWV-MALACAAPPIAGW-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---HPL----FIWLKMRISKLVP----WMILGSLLYVSMICVFHSKYAGFMVPYFLR--- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                             348 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sealfon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pennie & Edmonds LLP
                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
8.1%; Score 123.5; DB 2;
20.8%; Pred. No. 4.9e-05;
ative 63; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stuart C.
Cloning and Expression of
Gonadotropin-Releasing Hormone Receptor
                                                                                                                                                                                                                                                                                                                                                                                       US/08/390,000A
                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                  6923-052
                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----SRY----IPEGLQCSC 149
                               Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-820-521-2
                                                               ; MOLECULE TYPE: US-08-820-521-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08820521 Patent No. 5942416 GENERAL INFORMATION:
Query Match
Best Local Similarity
                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: CDNA CLONE HNFDY20 THAT ENCODES TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216 RVPGRGAPISALLSILSELILYESHCMIKVFLSSLKEHIRREIFL----FFILVIGIYPS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 GIDYYTLKPEVNNE---SFVIYMFVVHFTIPMIIIFFCYGQLVFTVKEAAAQQQES-ATT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  148 FGENHAIMGVAFTWVMALACAAPPLAGW------SRY----IPEGLQCSC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 ----HPL----FIW----LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR--- 157
                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: GH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         272 GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/820,521 FILING DATE: 19-MAR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 709 Swedeland CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                             NAME: Han, William T
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                   FILING DATE
                                                                                                       TOPOLOGY:
                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                          TELEFAX: 610-270-4026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QKAEKEVTRMVIIMVIAFLICWVPYASVAFYIFTHQGSNFGPIFMTIPAFFAKSAAIY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGGFTSTLYTSLHGYFVFGPTGCNLEGFFATLGGEIALWSLVVLAIERYVVVCKPMSNFR 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -NPVIYIMMNKQF----RNCMLTTICC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: SmithKline Beecham Corporation 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mao,
                                                                                                                                                      401 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ganesh, Sathe
Fuetterer, Wendy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bergsma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
                                                                                                         linear
                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Diskette
                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Јоусе
   8.1%;
                                                                                                                                                                                                                                                                                               34,344
                                                                                                                                                                                            2:
                                                                                                                                                                                                                                                                                  GH50011
     Score 122.5; DB 2; Pred. No. 7.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298
                       Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-748-506-22
                                                                                                                                                         ; MOLECULE TYPE: protein US-08-748-506-22
 밁
                               δã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 22, Application US/08748506 Patent No. 6159707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                     Matches
                                                                                                      Query Match
                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Leydig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60601-6780
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 TLAI----QIFSFVAEFSVPLLIFLFAVLLLIFSLGR---HTRQMRNTVAGSRVPGRGAP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 QAGLVSVACWLLASAHCSVVYVIEFSGDISHSQ------GTNGTCYLEFRKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 ---ISKLVPWMILG---SLLYVSMIC--VFHSKYAGFMVPYFLRKFFSQNATIQ---KED 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 ANGMHWPLPFILCPLSG--FIFFTTIYL-TALFLAAVSIERFLSVAHPL--WYKTRPRLG 185
                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278 VAGILAATILNFLVCFGPYNVSHVVGYICGESPAWRIYVTLLSTLNSCVDPFVYYF 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  232 QLAILLPVRLEMAVVLFVVPLIITSYCYSRLVWILGRGGSHRRQRR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 ISALL--SILSFLILY----FSH-----C-----MIKVFLSSLKFHIRRFIFLF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 FLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 08-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: Two Pa
                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 6 FILING DATE: 09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                   7.9%; Score 120.5; DB 3;
Local Similarity 23.4%; Pred. No. 9.2e-05;
Nes 64; Conservative 48; Mismatches 110;
                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
 28
                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                     TELEPHONE:
                               5 HL-IIYELLAVIQELLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLS-----CLAVSRIF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I----FFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKMR---- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLRILFFLLHLLAYLASLMGNMLIITITCVD---HRLQTPMYFFLSMFSSVECCFITTVI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71;
                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                       312-616-5700
                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                        312-616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                               US 60/033,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/748,506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53; Mismatches
                                                                                                                                                                                                                                                                                                                                            74940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                            Indels
                                                                                                            Length 327;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79;
                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                              14;
```

```
ş
                                                       밁
                                                                                  Š
                                                                                                                     В
                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-748-506-23; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        дЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                     Matches
                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                           TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atent No. 6159707
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: 1-0-0-1-1
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312-616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION UDATA:
US 60/033,751
FILING DATE: 09-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NOVE
111 RHPLEIWLKMRISKLVPWMILGSLLYVS-MICVFHSKYAG-FMVPVFLRKFFSQNATIQK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 150
                                                         85
                                                                             58 LQLFIFYVNVIVIF----FIEFIMCSANCAILLFINELELWLATWLGVF----YCAKVASV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196
                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137 HYPTIMSPRMCFLLVTVSLVLGFLFMASPVVMLSQSFYCGPNIIPHFFCD-FGPLANLSC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 RHPLFIWLKMRISKLVPWMILGSLLYVS-MICVFHSKYAG-FMVPYFLRKFFSQNATIOK 168
                                                                                                                                                                                   Local Similarity 23.4 les 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                             5 HL-IIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLS-----CLAVSRIF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 08-NOV
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60601-6780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Leydig, Voit & Mayer, Ltd. STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
                                                                                                              HLRILFFLLHLLAYLASLMGNMLIITITCVD---HRLQTPMYFFLSMFSSVECCFITTVI 84
                                              PQLL----TIILSGRQKIPFMACISQAFVYLVVGATGFFL---LGVLSLDRFLAICKPL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SETRSIEMLFFTL----AIIVLFASLLIAIFAYS-----NIVVTIVRLPSARERQRA- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDTLAIQIFSFVAEFSVPLLIFLFAVLLL-IFSLGRHTRQMRNTVAGSRVPGRGAPISAL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PQLL-----TIILSGRQKIPFMACISQAFVYLVVGATGFFL----LGVLSLDRFLAICKPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LQLFIFYVNVIVIF----FIEFIMCSANCAILLFINELELWLATWLGVF----YCAKVASV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3, Application US/08748506
6159707
                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----FSTCSSHLIVLSLMYGSCAFIYL 266
                                                                                                                                                                                                                                                                                                                                   327 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-1996
                                                                                                                                                                                                   7.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/08/748,506
                                                                                                                                                                                                                                                                                                                                                                  23:
                                                                                                                                                                                     48;
                                                                                                                                                                                                                                                                                                                                                                                                                                74940
                                                                                                                                                                                Score 120.5; DB 3;
Pred. No. 9.2e-05;
8; Mismatches 110;
                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                             Length 327;
                                                                                                                                                                                 Indels
                                                                                                                                                                                 51;
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136
                                                                                                                                                                                14;
```

```
á
                                                                    B
                                                                                            οy
                                                                                                                                В
     밁
                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-785-928-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-785-928-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (716)
INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                    125
                                                            106 MFLFPNIISTGLCRLEIFF----YYLYVYLDIFSVVCVSLVRYLLVAYSTRSWPK---KQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
159 SLGWYLTSAALLIALVLSGDACRHRSRVVD---PVSKQAMCYENAGNMTADWRLHVRTVS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137
                                                                                                                           53 ILSLI-FLINVLGNGLVTYI----FCKHRSRAGAIDILLLGICLNSLCLSISL--LAEVL
                                                                                                                                                          11 LLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMA-PLDLLLSCLAVSRIFLQLFIFYVNVIV 69
                                                                                                                                                                                                             Match 7.98;
Local Similarity 22.48;
                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 22-JAN CLASSIFICATION: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                             LVPWMILGSLLYVSMI-----CVFHSKYAGFMVPYFLRKFFSQNATIQKED-TLAIQIFS 178
                                                                                          IFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFI-----WLKMRISK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SETRSIEMLFFTL-----AIIVLFASLLIAIFAYS-----NIVVTIVRLPSARERQRA- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDTLAIQIFSFVAEFSVPLLIFLFAVLLL-IFSLGRHTRQMRNTVAGSRVPGRGAPISAL 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPTIMSPRMCFLLVTVSLVLGFLFMASPVVMLSQSFYCGPNIIPHFFCD-FGPLANLSC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14603
                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Goldman, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rochester
: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08785928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clinton Square,
                                                                                                                                                                                                                                                                                                                                                            342 amino acids
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cesarman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Geras-Raaka, Elizabeth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gershengorn, Marvin C
Arvanitakis, Leandros
                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                          (716)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nixon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FSTCSSHLIVLSLMYGSCAFIYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                        263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                      263-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONSTITUTIVELY ACTIVE G PROTEIN COUPLED RECEPTOR OF HHV 8 AND METHOD OF IDENTIFYING NEGATIVE ANTAGONISTS OF G PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hargrave, Devans & Doyle LLP
| Juare, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ethel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/785,928
                                                                                                                                                                                           56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          19603/1320
                                                                                                                                                                                                            Score 120.5; DB 3 Pred. No. 9.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             266
                                                                                                                                                                                                                         DB 3;
                                                                                                                                                                                              95;
                                                                                                                                                                                            Indels 53;
                                                                                                                                                                                                                         Length 342;
                                                                                                                                                                                         Gaps
                                                                                                                             105
                                                             158
                                                                                                                                                                                            14;
```

Qy В δÃ

밁

; Sequence 17, Application
; Patent No. 6093806
; GENERAL INFORMATION:
APPLICANT: Cesarman,
APPLICANT: KNOWNES, D
APPLICANT: KNOWNES, D

Cesarman,

CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES: TITLE OF INVENTION:

ADDRESSEE:

STREET: CITY: Rochester

New York

COMPUTER READABLE FORM:

14603

MEDIUM TYPE:

COUNTRY:

USA

RESULT 8 US-08-728-603-17

```
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,603
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 FVAEFSVPLLIFLFAVLLLIFSLG----RHTR-QMRNTVAGSRVPGRGAPISALLSILSF 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 VTAGFLLPL----ALLILFYALTWCVVRRTKLQARRKVRG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  257 VLLFFVFCFPYHVLNLLDTLLRR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 LILYFSHCMIKVFLSSLKFHIRR 256
                                                                                                                                                                                       106 MFLFPNIISTGLCRLEIFF----YYLYVYLDIFSVVCVSLVRYLLVAYSTRSWPK---KQ 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BRAMAN, SUSAN J.
REGISTRATION NUMBER: 34,103
REFERENCE/DOCKET NUMBER: 19
234 LILYFSHCMIKVFLSSLKFHIRR 256
                                                                                                                                                125 LVPWMILGSLLYVSMI-----CVFHSKYAGFMVPYFLRKFFSQNATIQKED-TLAIQIFS 178
                                                                                                                                                                                                                                                                  53 ILSLI-FLINVLGNGLVTYI----FCKHRSRAGAIDILLLGICLNSLCLSISL--LAEVL 105
                                                                                                                                                                                                                                                                                                   11 LLAVIQFILGIFTNGIIVVVNGIDLIKHRKMA-PLDLLLSCLAVSRIFLQLFIFYVNVIV 69
                                                                       FVAEFSVPLLIFLFAVLLLIFSLG----RHTR-QMRNTVAGSRVPGRGAPISALLSILSF 233
                                                                                                              SLGWVLTSAALLIALVLSGDACRHRSRVVD---PVSKQAMCYENAGNMTADWRLHVRTVS 215
                                                                                                                                                                                                                            IFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFI-----WLKMRISK 124
                                    VTAGFLLPL----ALLILFYALTWCVVRRTKLQARRKVRG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08728603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: NIXON, HARGRAVE, DEVANS & DOYLE LLP
Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                              7.9%; Score 120.5; DB 3; 22.4%; Pred. No. 9.7e-05; ative 56; Mismatches 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Daniel M.
PROTEINS OF KAPOSI'S SARCOMA ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HERPESVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ethel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19603/720
                                                                                                                                                                                                                                                                                                                                                                                      .Length 342;
                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----VIVAV 256
                                            ---VIVAV 256
                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-928-692-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                        망
                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: li
; MOLECULE TYPE:
US-08-928-692-12
                                                                                                                                            Š
                                                                                                                                                                                   밁
                                                                                                                                                                                                                        8
          US-08-466-103A-2
; Sequence 2, Application US/08466103A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1.
Patent No.
                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: (CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                      304 ILVALMLHVAQQFSGI--NGIFYYSTSIFQTAGIS-----KPVYATIGVGAVNNVFTA 354
                                                                                                         437
                                                                                                                                            173 AIQIFS-----
                                                                                                                                                                                     387
                                                                                                                                                                                                                   120 MRISKLVPWMILGSLLYVSMICVFHSKYAGFM-----VPYFL-RKFFSQNATIQKEDTL 172
                                                                                                                                                                                                                                                              355 VSVFLVEK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET_NUMBER: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 12-SEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                 60 LFIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                          6 LIIYFLLAVIQELLGIFTNGI-----IVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLLFFVFCFPYHVLNLLDTLLRR
                                                                                                                                                                                   LVLLNKFSWM-----SYVSMIAIF--LFVSFFEIGPGPIPWFMVAEFFSQG---PRPAAL 436
                                                                                                     AIAAFSNWTCNFIVALCFQYIADFCGPYVFFLFAGVLLAFTL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New York
                                                                                                                                                                                                                                                                                                                                                                                                                   1 Similarity
55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08928692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 405 Lexington Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               524 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212-878-9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yaver, Deborah
Lamsa, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brody,
                                                                                                                                                                                                                                                                                                                                                                                                               7.8%; Score 118.5; DB 2 clarity 24.8%; Pred. No. 0.00026; Conservative 30; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 59587270 No. 5958727disk of No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-SEPT-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No. 5958727e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methods for Modifying the Production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a Polypeptide
80
                                                                                                                                              ----FVAEFSVPLLIFLFAVLLLIFSL 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/928,692
                                                                                                                                                                                                                                                                -----AGRRSLFLIGMSGMFVCA-----IFMSVG 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4944.200-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5958727th America, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                         Indels 73;
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
```

; TOPOLOGY: 1i ; MOLECULE TYPE: US-08-728-603-17

STRANDEDNESS:

linear protein

11;

amino acid

TELEFAX: 716-263-1600 INFORMATION FOR SEQ ID NO:

716-263-1600

TELEPHONE:

SEQUENCE CHARACTERISTICS: LENGTH: 342 amino acid

Query Match Best Local Similarity

Matches

Conservative

Ş , 명 Ş 무 Ş

밁

Š 뫄 δÃ

```
US-08-748-506-24
                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.8%; Score 118; DB 2; Length 420; Best Local Similarity 19.4%; Pred. No. 0.00022; Matches 57; Conservative 64; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/466,103A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/319,887
FILING DATE: 07-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: 08/261,857
FILING DATE: 17-JUN-1994
ATTOREY/AGENT INFORMATION:
ANAME: TRAIN TOOR ATTOREY
ANAME: TRAIN TOOR ATTOREY
ANAME: TRAIN TOOR ATTOREY
ANAME: TRAIN TRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 5856124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617/542-8906 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                      256 WAPLNFIGLAVAINPFHVAPKIPEWLFVLSYFMAYFNSCLNAVIYGVLNQNFRK 309
                                                                                                                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                      175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 RISKLV----PWMILGSLLYVSMICVFHSKYAGFMV--PYFLRKFFSQNATIQKEDTLAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reppert, Steven M.
APPLICANT: EDISAWA, TAKASHI
TITLE OF INVENTION: HIGH-AFFINITY MELATONIN
TITLE OF INVENTION: RECEPTORS AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 FIFYVNVIVIFFIBFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 LTSALAVVLIFTIVVDVLG----NTLVI---LSVLRNKKLQNAGNLFVVSLSIADLVVAV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson P.C. STREET: 225 Franklin Street
                                                                                                                                                                                                                           -----GSRV---PGRGAP-ISALLSILSFLILYFSHCMIKVFLSSLKFHIRR 256
                                                                                                                                                                                                                                                                                                         VVVHFIVPLSVVTFCYL-RIWVLVIQVKHRVRQDFKQKLTQTDLRNFLTMFVVFVLFAVC
                                                                                                                                                                                                                                                                                                                                                                                  QIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQ-----MRNTVA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                               RYDKLYNQRSTWCYLGLTWILTIIAIVPNFFVGSLQYDPRIFSCTFAQ--TVSSSYTITV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YPYPVILIAIFQNGWTLGNIHCQISGFLMGLSV----IGSVFNITAIAINRYCYICHSL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPL-DLLLSCLAVSRIFLQL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΜA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Windows95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00786/250002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                      213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
```

```
В
                                             Ş
                                                                                        밁
                                                                                                                               Q
                                                                                                                                                                            В
                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein US-08-748-506-24
                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 7.7%; Score 117.5; DB 3; Length 327; Best Local Similarity 22.1%; Pred. No. 0.00019; Matches 60; Conservative 51; Mismatches 112; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/748,506
FILING DATE: 08-NOV-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 24, Application US/08748506 Patent No. 6159707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-616-5700
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 312-616-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,751
FILING DATE: 09-NOV-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL SPERM RECEPTORS NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leyalig, Voit & Mayer, Ltd.
STREET: Two Prudential Plaza, Suite 4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NOVE
244 -----FSTCSSHLIVLSLMYGSCVFIYL 266
                             229 SILSFLILYFSHCMIKVFLSSLKFHIRRFIFL 260
                                                                                    199 RSIEMLFTLAIIVLFTSLLIAIFAYSTIVVTIVR-----
                                                                                                                                                                   140 TIMSPRMCFLLVTVSLVLGFLFMASPVVMLSQSFYCGPNIIPHFFCD-FGPLANLSCSET 198
                                                                                                                                                                                                            114 LFIWLKMRISKLVPWMILGSLLYVS-MICVFHSKYAG-FMVPYFLRKFFSQNATIQKEDT 171
                                                                                                                                                                                                                                                                                           58 LOLFIFYVNVIVIF---FIEFIMCSANCAILLFINELELWLATWLGV-FYCAKVASVRHP 113
                                                                                                                                                                                                                                                                                                                                         28 HLRILFFLLHMLAYLASSMGNMLIITYTCVD---HRLQTPMYFFLSTFSFVECCFITTVI 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: Two Pr
                                                                                                                                                                                                                                                                                                                                                                               5 HL-IIYELLAVIQELLGIETNGIIVVVNGIDLIKHRKMAPLDLLLS------CLAVSRIF 57
                                                                                                                        LAIQIFSFVAEFSV---PLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALL 228
                                                                                                                                                                                                                                                     PQLL----TIILSGRQKIPFMACFSQAFVVLFLGAAVFFLMAVLSLDRFLAICKPLHYP 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60601-6780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 25
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
```

12;

US-08-458-970A-11

Sequence 11, Application US/08458970A Patent No. 5861272

GENERAL INFORMATION: APPLICANT: LI, ET

APPLICANT: LI, ET AL.
TITLE OF INVENTION: (
NUMBER OF SEQUENCES:

C5a Receptor

CORRESPONDENCE ADDRESS:

ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN ADDRESSEE: CECCHI, STEWART & OLSTEIN

STREET:

6 BECKER FARM ROAD

```
δõ
                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                        Ъ
                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-458-970A-11
                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                   Š
                                                                                   RESULT 13
US-08-118-270-65
                                                                                                                                                     В
                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                            Sequence 65, Application US/08118270 Patent No. 5508384 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09234
FILING DATE: 16 AUG 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                          139 RTMLVAKVTCIIIWLLAGLASL-PAIIHRNVFFIENTNITVCAFHYESQNSTLPIGLGLT 197
                                                                                                                                                                                                                                                                                                                                                                                             114 -----LFIWLKMRISKLVPWMILGSLLYVS----MICVFH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/458,970A FILING DATE: June 2, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: UZIP: 07068
 APPLICANT:
                                                                                                                                                     301 YGFLGKKFKRY-FLQLLKYIPPKAKSHS 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MULLINS, J.G. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                             82 LWAVYTAMEYRWPFGNYLCKIASASVSFNLYASVFLLTCLSI---DRYLAIVHPMKSRLR 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 IFYVNVIVIFFIEF--IMCSANCAILLFINELELWLATWLGVFYCAKVASVRHP----- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 HNYIFVMIPTLYSIIFVVGIFGNSLVVIVIYF-YMKLKTVASVFLLNLALADLCFLLTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLIIYFLLAV---IQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLF 61
                                                                                                                                                                                                                                                                                         KNILGFLFPFLIILTSYTLIWKALKKAYEIQKNKPRNDDIFKIIMAIVLFFF---FSWIP 254
                                                                                                                                                                                                                                                     LLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISALLSILSFLILYFSHCMIKVF 246
                                                                                                                                                                                                                                                                                                                        SKYAGFMVPYF------LRKFFSQNATIQKED----TLAIQIFSFVAEFS-VP 186
                                                                                                                                                                                      LSSLKFHIRRFIFLFFILVIGIYPSGHS 274
                                                                                                                                                                                                                        HQIFTFLDVLIQLGIIRDCRIA - - DIVDTAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROSELAND
REW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201-994-1744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: MS-DOS
WORD PERFECT 5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PS/2
Murphy, Randall Schuster, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33,073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                325800-353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 113.5; DB 2
Pred. No. 0.00053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122;
                                                                                                                                                                                                                            -ITICIAYFUNCLUPLF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
```

```
ρ
                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                           밁
                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-118-270-65
                                                             밁
                                                                                         S
                                                                                                                           밁
                                                                                                                                                          δõ
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MU
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 41.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                        176 IFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS---RVP---GRGAPISALLS 229
                                                                                                                                                                                         108 VIVSSRIZVLGSW---AGGEGISMVKVFLISRLSYCGPNTINHFFC-----DVSPLL 156
                                                                                                                                                                                                              TELEPHONE: 202 - 3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/118,270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                          208 HLTVVIIFYA---ASIFIYARPKALSAFTDNKLVSVLYAVIVPLFNPIIYCLRNQDVKRA 264
                                                                                         230 ILSFLILYFSHCMIKVFLSSLKFHIRRFI--FLFFILVIGIYPSGHSLILILGNPKLKQN 287
265 LRRTL 269
                             288 AKKFL 292
                                                                                                                                                                                                                                                         48 TIPKLMGFIGSKENHGQLISFFACMTQLYFFLGLGCTECVLLAVMAYDRYVAICHPLHYP 107
                                                                                                                                                                                                                                                                                    68 IVIFFIEFINCSANCAILL--FINELELWLATWLGVFYCAKVA------SVRHPLF-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                    8 IYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNV 67
                                                                                                                                                                                                                                                                                                                      1 LLFFLSLLXYVLVLTENMLIIIAIRNHPTLHKPM------YFFLFLEIWYVTV
                                                                                                                           NLSCTDMSTAELTDFVIAIFILLGPL-----SVTGASYMRIPSAAGRHKAFSTCAS
                                                                                                                                                                                                                                                                                                                                                                                        66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Townsend, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  בא: single
linear
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-199
                                                                                                                                                                                                                                                                                                                                                                                      7.0%; Score 107; DB 1; Length 286; 21.6%; Pred. No. 0.0019; rative 52; Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/943,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MURPHY-2A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 25
                                                                                                                                                                                                                                                                                                                                                                                              56;
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                 47
                                                                                                                                    207
                                                                                                                                                                                                                                                                                                                                                                                                11;
```

PCT-US93-08528-65 , Sequence 65, Application PC/TUS9308528 ; GENERAL INFORMATION: , APPLICANT: New York University

RESULT

```
RESULT 15
US-08-148-209A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
Sequence 4, Application US/08148209A Patent No. 5556780 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US FILING DATE: 09-SEP-1993 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPAX: 202-737-3528
TELEX: 246633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 286 amino acid
                                                                                                                                                                                                                                                                                                   265 LRRTL 269
                                                                                                                                                                                                                                                                                                                                                                             288 AKKFL 292
                                                                                                                                                                                                                                                                                                                                                                                                                                            208 HLTVVIIFYA---ASIFIYARPKALSAFTDNKLVSVLYAVIVPLENPIIYCLRNQDVKRA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 ILSFUILYFSHCMIKVFLSSLKFHIRRFI--FLFFILVIGIYPSGHSLILILGNPKLKQN 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 NLSCTDMSTAELTDEVIAIFILLGPL-----SVTGASYMRIPSAAGRHKAFSTCAS 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 IFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS---RVP---GRGAPISALLS 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 IWLKMRISKLVPWMILGSLLYVSMICVFHSKYAGFWVPYFLRKFFSQNATIQKEDTLAIQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PO
TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68 IVIFFIEFIMCSANCAILL--FINELELWLATWLGVFYCAKVA-----SVRHPLF-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
mes 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LLFFLSLLXYVLVLTENMLIIIAIRNHPTLHKPM------YFFLFLEIWYVTV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VIVSSRIZVLGSW---AGGFGISMVKVFLISRLSYCGPNTINHFFC------DVSPLL 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIPKLMGFIGSKENHGQLISFFACMTQLYFFLGLGCTECVLLAVMAYDRYVAICHPLHYP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNV 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      i: 286 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Townsend, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SS: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.0%; Score 107; DB 4; Length 286; 21.6%; Pred. No. 0.0019; rative 52; Mismatches 131; Indels 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/943,236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCT/US93/08528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
```

```
Q
                                                                                  밁
                                                                                                                  Q
                                                                                                                                                                В
                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEER: (415)
TELEX: 910 277299
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
**FNGTH: 359 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.9%;
Best Local Similarity 21.3%;
Matches 70; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: ROwland, Bertram I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mukoyama, Masashi
TITLE OF INVENTION: TYPE-2 ANGIOTENSIN II RECEPTOR AND GENE
NUMBER OF SEQUENCES: 16
301 FYGFLGKKFKKY-FLQLLKYIPPKAKSHS 328
                                                                                256 HQIFTF--LDVLIQLGVIHDCKIAD-IVDTAMP-----
                                                                                                                                                          199 KNILGFLFPFLIILTSYTLIWKALKKAYEIQKNKPRNDDIFRIIMAIVLFFF---FSWVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                  83 LWAVYTAMEYRWPFGNHLCKIASASVSFNLYASVFLLTCLSI---DRYLAIVHPMKSRLR 139
                                                                                                                                                                                                                                                                                                                                                      62 IFYVNVIVIFFIEF--IMCSANCAILLFINELELWLATWLGVFYCAKVASVRHP----- 113
                                                                                                                                                                                                                                                                                                                                                                                              24 HSYIFVMIPTLYSIIFVVGIFGNSLVVIVIYF-YMKLKTVASVFLLNLALADLCFLLTLP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-58491-1/BIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 4 Embarcade:
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                  5 HLIIYFLLAV---IQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 05-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                        FLSSLKFHIRRFIFLFFILVIGIYPSGHS 274
                                                                                                               LLIFLFAVLLLIFSLG-RHTRQMRNTVAGSRVPGRGAPISALLSILSFLILYFSHCMIKV 245
                                                                                                                                                                                              SKYAGFWVPYF-----LRKFFSQNATIQKED----TLAIQIFSFVAEFS-VP 186
                                                                                                                                                                                                                                      RTMLVAKVTCIIIWLMAGLASL-PAVIHRNVYFIENTNITVCAFHYESRNSTLPIGLGLT 198
                                                                                                                                                                                                                                                                                California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dzau, Victor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     יס: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/148,209#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 104.5; DB 1; Length 359; Pred. No. 0.0044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118; Indels
                                                                            ITICIAYFUNCLUPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83;
                                                                                                                                                          255
                                                                                                                                                                                                                                                                            144
```

17;

Search completed: March 15, Job time: 4696 sec

2001, 12:57:20

THIS PAGE BLANK (USPTO)

```
Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
                                          pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein search, using sw model
                                                                                                                                                                                                                                                                  10:
11:
12:
13:
14:
15:
16:
16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-510-332-1
1521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        March 15, 2001, 12:32:39; Search time 76.8 Seconds
                                                                                                                                                            18:
19:
20:
21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MLESHLIIYFLLAVIQFLLG......GNPKLKQNAKKFLLHSKCCQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268485 seqs, 34193795 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cgn2_2/gcgdata/geneseq/geneseqp/AA1980 DAT:*
/cgn2_2/gcgdata/geneseq/geneseqp/AA1981 DAT:*
/cgn2_2/gcgdata/geneseq/geneseqp/AA1982 DAT:*
/cgn2_2/gcgdata/geneseq/geneseqp/AA1983 DAT:*
/cgn2_2/gcgdata/geneseq/geneseqp/AA1984 DAT:*
/cgn2_2/gcgdata/geneseq/geneseqp/AA1985 DAT:*
/cgn2_2/gcgdata/geneseq/geneseqp/AA1985 DAT:*
/cgn2_2/gcgdata/geneseq/geneseqp/AA1985 DAT:*
                                                                                                                                                                                                                                                                                                                                       /cgn2_2/gcgdata/geneseq/geneseqp/AA198 DAT: *
/cgn2_2/gcgdata/geneseq/geneseqp/AA198 DAT: *
/cgn2_2/gcgdata/geneseq/geneseqp/AA1990 DAT: *
/cgn2_2/gcgdata/geneseq/geneseqp/AA1991 DAT: *
/cgn2_2/gcgdata/geneseq/geneseqp/AA1992 DAT: *
/cgn2_2/gcgdata/geneseq/geneseqp/AA1992 DAT: *
                                                                                                                                                                                /cgn2_/gcgdata/genesed/genesedp/Aa1993.DAT:*
/cgn2_/gcgdata/genesedy/genesedp/Aa1994.DAT:*
/cgn2_/gcgdata/genesedy/genesedp/Aa1994.DAT:*
/cgn2_/gcgdata/genesedy/genesedp/Aa1995.DAT:*
/cgn2_/gcgdata/genesedy/genesedp/Aa1997.DAT:*
/cgn2_/gcgdata/genesedy/genesedp/Aa1998.DAT:*
/cgn2_/gcgdata/genesedy/genesedp/Aa1998.DAT:*
/cgn2_2/gcgdata/genesedy/genesedp/Aa1999.DAT:*
                                                                                                                                                   /cgn2_2/gcgdata/geneseq/geneseqp/AA2000.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gcgdata/geneseq/geneseqp/AA1986
SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (without alignments)
133.124 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .DAT:*
```

Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
1	263.5	17.3	256	20	Y42388	Amino acid sequenc
2	124.5	8.2	348	14	R38483	Rhodopsin protein.
ω	124.5	8.2	348	17	R93116	Rhodopsin. Homo s
4	123.5	8.1	309	15	R48735	G-protein coupled
_ر	123.5	8.1	309	17	W02707	G-protein coupled
6	122.5	8.1	401	19	W59924	Human 7-transmembr
7	120.5	7.9	342	19	W37976	Kaposi's sarcoma a
89	118	7.8	354	18	W25926	Xenopus melatonin
9	118	7.8	354	18	W25927	Xenopus melatonin
10	118	7.8	420	17	R88409	High-affinity mela
11	117.5	7.7	310	18	W19105	Rat pheromone rece
12	117.5	7.7	522	18	W17836	Rat glucose transp

4444449336434 544444494 54444449	
117.5 117.5 114.5 112.5 112.5 112.5 1109.5 109.5 109.5 109.5 109.5 109.5 109.5 107.5 107.5 107.5 107.5 107.5 107.5 107.5 107.5 107.5 107.5 107.5 108.5 109.5	
55555555555555555555555555555555555555	ļ
349 123 354 476 476 449 3449 3449 3449 347 317 317 317 317 317 317 317 31	•
200 200 200 200 200 200 200 200 200 200	,
Y83524 Y83524 Y87554 P90554 Y77057 Y1908 Y1908 Y19908 Y19908 Y19908 Y19908 Y19908 Y19908 Y19908 W85716 W85716 W85716 W85716 W85716 W85716 Y9383 W19108 W12243 W19108 Y19183 Y1918	,
proc288 polypeptide Bovine rhodopsin. Human secreted pro Rhodopsin amino ac Staphylococcus aur Human Putative Adr B. burgdorferi ant B. burgdorferi ant Human G protein coupled G-protein coupled G-protein coupled G-protein coupled Kidney injury asso Guinea pig platele Rat spermatid chem Amino acid sequenc Human 7-transmembr Guinea pig platele Seven transmembran Human 70 seven tr G protein-coupled G-protein coupled G-protein coupled G-protein-coupled G-protein-coupled G-protein-coupled G-protein-coupled G-protein-coupled Human ADV receptor Human G protein-co Peptide Seq ID No: Human lectomedin-1 Human lectomedin-1 Human lectomedin-1	, ,

ALIGNMENTS

RESULT 1 Y42388 ID Y42388 standard; Protein; 256 AA. XX FT FT FT FT FT FT XXX secreted protein; cDNA library; clone; transmembrane protein; signal sequence cloning; hybridization cloning; gene therapy; 09-DEC-1999 (first entry) Y42388; receptor. Amino acid sequence of pt127_1. Key 18-FEB-1998; 17-FEB-1999; 26-AUG-1999 W09942470-A1. Misc-difference Protein Homo sapiens. (GEMY) GENETICS INST INC. 18-FEB-1999; Peptide 98US-0075038. 99US-0251600. 99WO-US03458 /label= Leader/Signal peptide 21..256 Location/Qualifiers /label= Unknown /note= "encoded by twa" /label= Mature protein

```
RESULT
R38483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                      망
                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                           õ
                                                                                                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                            Š
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Sin
Matches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity, cytokine and cell proliferation/differentiation activity, limmune stimulating (e.g. as vaccines) or suppressing activity, hematopoiesis regulating activity, tissue growth activity, hemostatic activity, hemostatic and thrombolytic activity, chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumor invasion suppressor activity, and tumor inhibition activity. The PNs are also stated to be useful for gene therapy. Other activities include inhibiting the growth, infection or function of bacteria, fungi, viruses and other parasites; effecting bodily characteristics such as e.g. weight, color, skin, etc., effecting biorhythms or caricadic cycles; enhancing fertility; treatment of depression; treatment of pain; hormonal or endocrine activity.
                                                                            11-NOV-1993
                                                                                                    R38483;
              hereditary.
                          Human; rhodopsin;
                                                 Rhodopsin protein
                                                                                                                           R38483 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the amino acid sequence of the pt127_1 protein, which is derived from the pt127_1 clone isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA ilbrary.

The PNS and proteins of the invention are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jacobs
Treacy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding human secreted proteins used therapeutic, diagnostic and research purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-518580/43
                                                                                                                                                                                          222
                                                                                                                                                                                                                 224
                                                                                                                                                                                                                                          170
                                                                                                                                                                                                                                                                 168
                                                                                                                                                                                                                                                                                         121
                                                                                                                                                                                                                                                                                                                 118
                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                   dpthlsdmtvttlan1-ipftlsllsflllicslckhlkkm-----qfhgkgspdsnt 221
                                                                                                                                                                                                                                                                                                                                                                                               IIYFLLAVIQELLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVN 66
                                                                                                                                                                                        kvhikalqtvtsflllf 238
                                                                                                                                                                                                                ---ISALLSILSFLILY 237
                                                                                                                                                                                                                                                            KEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAP----
                                                                                                                                                                                                                                                                                      lkrriksvipvillgsllf--lvchlvvvnmdesmwtkeyegnv-
                                                                                                                                                                                                                                                                                                            LKMRISKLVPWMILGSLLYVSMIC------VFHSKYAGFMVPYFLRKFFSQNATIQ 167
                                                                                                                                                                                                                                                                                                                                                           VIVIFFIEFIMCSANCAILLFI-----NELELWLATWLGVFYCAKVASVRHPLFIW 117
                                                                                                                                                                                                                                                                                                                                                                                 iifsilvvvtfvlgnfangfivlvnsiewvkrqkisfadqiltalavsrvgl-----lw 60
                                                                                                                                                                                                                                                                                                                                    vilxhwyatvlnpgsyslgvrittinawavtnhfsiwvatslsifyllkianfsnfiflh 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ح ح
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McCoy JM,
Agostino I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    256
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                        mutant; retinal degeneration; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          걸
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.3%; Score 263.5;
28.8%; Pred. No. 7.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LaVallie ER,
MJ, Steininger
                                                                                                                           348 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collins-Racie LA, RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  .9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                     74;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                     ----sweikls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Merberg D;
                        probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                    51;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    80
RESULT
R93116
ID R9
XX
AC R9
XX
DT 06
                                                                                                                         밁
                                                                                                                                             õ
                                                                                                                                                                       밁
                                                                                                                                                                                              Š
                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                            Q
                                                                                                                                                                                                                                                                      ₽
                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                       B
                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                     Вþ
                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
           06-JUL-1996
                                                          R93116 standard;
                                    R93116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 56pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berson EL, Dryja TP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hereditary retinal degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HARD ) HARVARD COLLEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-DEC-1992;
                                                                                                                         302
                                                                                                                                                272
                                                                                                                                                                                                                         188
                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUN-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9312134-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                         244
                                                                                                                                                                                                                                                                                                                                               60
                                                                                    ω
                                                                                                                      -npviyimmnkqf----rncmltticc 323
                                                                                                                                             GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1993-214088/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      68;
                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q43543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0805123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92WO-US10536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 249
                                                          Protein;
```

The sequence given represents the human rhodopsin protein. Mutant rhodopsin proteins cause retinal degeneration. The DNA encoding the mutant DNA sequences may be identified using primers/probes described in the invention (see also 043345-48) and may be used to diagnose Probe or primer contg. sequence of human retinal degeneration slow protein mutant - used to diagnose hereditary retinal degenerative diseases 39 mlaaym---fliivlgfpinfltlyvtv------qhkklrtplnyillnlavadlfmv 1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ gidyytlkpevnne---sfviymfvvhftipmiiiffcygqlvftvkeaaaqqqes-att ----HPL----FIW----LKMRISKLVPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111 RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS lggftstlytslhgyfvfgptgcnlegffatlggeialwslvvlaieryvvvckpmsnfr fgenhaimgvaftwvmalacaapplagw-----sry----ipeglqcsc 187 /note= "Sequence unclear at this position" 8.2%; Score 124.5; DB 1 20.8%; Pred. No. 2.1e-06; tive 63; Mismatches 125 DB 14; 125; Length 348; Gaps 271 147 59 301 157 87 16;

```
δ.
                                                                                            밁
                                                                                                                                                  В
                                                                                                                                                                            Ş
                                                                                                                                                                                                                                  δÃ
             Š
                                        밁
                                                               QΥ
                                                                                                                                                                                                     ٩
                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-1993;
24-JAN-1990;
11-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                         This sequence represents human rhodopsin, and is encoded by sequences T17115 (without introns) and T17116 (with introns). Substitution of histidine for the normal nonpolar amino acid proline at position 23 results in a dysfunctional or absent molecule, affecting rod function, and is linked with autosomal dominant retinitis pigmentosa. Probes and primers specific for this mutation may be used as diagnostic agents. Mutations in the cGMP-phosphodiesterase genes are also implicated in retinitis pigmentosa. Detection of any of these mutations in a foetus or patient may be used in diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Diagnosis of hereditary retinal degenerative diseases e.g. retinitis pigmentosa, - caused by a human photoreceptor protein mutation, by detection of the mutation by PCR amplification or hybridisation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; rhodopsin; transversion; mutation; retinitis pigmentosa;
probe; primer; hybridisation; polymerase chain reaction; PCR;
eye; rod; retina; diagnostic; prenatal diagnosis; photoreceptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5498521-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HARD ) HARVARD COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methods
                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                           112
               216
                                          188
                                                                                               148
                                                                                                                                                    88
                                                                                                                                                                               60
                                                                                                                                                                                                           39
                                                                                                                                                                                                                                   1 MLESHLITYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1996-159684/16.
DB; T17115, T17116.
                                                                                                                                                                                                         mlaaym---filivlgfpinfltlyvtv-----qhkklrtplnyillnlavadlfmv
RVPGRGAPTSALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS::::::|||::::|||::||
                                        gidyytlkpevnne---sfviymfvvhftipmiiiffcygqlvftvkeaaaqqqes-att
                                                                                                               ----HPL----FIW---LKMRISKLYPWMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                               fgenhaimgvaftwvmalacaapplagw------
                                                                                                                                                    lggftstlytslhgyfvfgptgcnlegffatlggeialwslvvlaieryvvvckpmsnfr
                                                                                                                                                                              LFIFYVNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EL,
                                                                                                                                                                                                                                                                  68;
                                                                 KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Column 19-24; 71pp;
                                                                                                                                                                                                                                                                                                                                     348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dryja TP;
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93US-0033081.
90US-0469215.
91US-0805123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0469215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Mutated to His
                                                                                                                                                                                                                                                                            8.2%;
                                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                                               Score 124.5; DB : Pred. No. 2.1e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     retinitis
                                                                                                                                                                                                                                                                                            DB 17;
                                                                                                                                                                                                                                                                   125;
                                                                                               -sry----ipeglqcsc
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pigmentosa"
                                                                                                                                                                                                                                                                                             348;
                                                                                                                                                                                                                                                                   71;
                                                                                                                                                                                                                                                                  Gaps
                 271
                                            243
                                                                       215
                                                                                                  187
                                                                                                                                                      147
                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                   16;
```

```
RESULT
R48735
                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δδ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뮹
                                                      Qy
                                                                                     В
Š
                             밁
                                                                                                                QY
                                                                                                                                                  Matches
                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                proteins selected from cAMP, adenosine, muscarinic acetylcholine, proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin adrenergic, tytomegaloviral and other G-protein coupled receptors. The receptor proteins were used to design polypeptides, pref. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see R48759-R48758, R50569-R50807 and R89189-R89195 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related ta GPR abnormality e.g. a psychotic disorder such as schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 G-protein coupled receptor; ligand binding assay; transmembs psychotic disorder; schizophrenia; dopamine; cAMP; adenosing muscarinic acetylcholine; adrenergic; endothelin; bombesin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R48735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9405695-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rhodopsin; opsin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R48735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murphy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 111-112; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptides of G-coupled receptor proteins (binding GPR ligands or modulating GPR binding
                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                    Proteins R48685-R48758 represent a range of G-protein coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    244
 112
                               51
                                                           60
                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qkaekevtrmviimviaflicwvpyasvafyifthqgsnfgpifmtipaffaksaaiy--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -npviyimmnkqf----rncmltticcr 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHSLILILGNPKLKQNAKKFLLHSKCCQ 299
: :| |: |: : | : ||:
                                                         LFIFYVNVIVIFFIEFIMCSANCAILLFINEL-----ELWLATWLGVFYCAKVASVR- 111
                                                                                       mlaaym---fllivlgfpinfltlyvtv-----qhkklrtpinyillnlavadlfmv
                                                                                                                  MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1994-101120/12
                          lggftstlytslhgyfvfgptgcnlegffatlggeialwslwlaieryvvvckpmsnfrf 110
---HPL----FIWLKMRISKLVP----WMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RB,
                                                                                                                                                  69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coupled
                                                                                                                                                                                                                          309
                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                          ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92US-0943236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93WO-US08528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      odorant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human rhodopsin protein.
                                                                                                                                                               8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytomegalovirus.
                                                                                                                                                  64;
                                                                                                                                                               Score 123.5; DB 1
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹
                                                                                                                                                  Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dopamine; cAMP; adenosine; ti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GPRs) -
                                                                                                                                                                                  15;
                                                                                                                                                      Indels
                                                                                                                                                                               Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful
                                                                                                                                                    73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endocrine;
                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301
                                                                                            50
                                                                                                                        59
                                                                                                                                                                                                                                                                           ç
                                                                                                                                                       17;
```

```
RESULT
W02707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                     Query Match
Best Local !
         Matches
                                                                                                         were used to design polypeptides, prof. based on the transmembrane domains, for use in G-protein coupled receptor ligand binding assays. The polypeptide fragments retain biological activity such as binding a GPR ligand or modulating GPR ligand binding to a GPR (see W0747-W02999 for examples of polypeptide fragments). The polypeptide fragments can be used in compositions for treating subjects suffering from a pathology related to a GPR abnormality e.g. a psychotic disorder such as
                                                                                                                                                                                                 Proteins W02657-W02730 represent a range of G-protein coupled receptor (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine, adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin odorant, cytomegaloviral and other GPR proteins. The receptor proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        schizophrenia; dopamine; cAMP;
muscarinic acetylcholine; endot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-protein coupled receptor; ligand binding assay; transmembrane domain; schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin;
                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                       WPI; 1996-208785/21.
                                                                                                                                                                                                                                                                                                                                                                                                                    09-SEP-1993;
10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G-protein
                                                                                                 schizophrenia.
                                                                                                                                                                                                                                                                                                                                                                                        (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5508384-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             odorant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W02707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W02707 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111
                    Local
                                                                                                                                                                                                                                                                                             dopamine receptor peptide - useful as antipsychotic agent, e.g. treating \operatorname{schizophrenia}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -npviyiifnkqf----rncmlqlicc 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qkaekevtrmviimviaflicwvpyasvafyifthqgsnfgpifmripaffaksaaiy--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genhaimgvaftwv-malacaappiagw------sry----ipeglqcsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS
        69; Conservative
                                                                                                                                                                                                                                                                                                                                                                 RB,
                                                                          309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coupled
                                                                                                                                                                                                                                                                   Column 139-140; 184pp; English.
                                                                                                                                                                                                                                                                                                                                                              Schuster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                        À
                                                                                                                                                                                                                                                                                                                                                                                                                 93US-0118270.
92US-0943236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         92US-0943236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human rhodopsin.
                 8.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cAMP; adenosine; thrombin; adrene;
endothelin; bombesin; endocrine;
serotonergic.
        64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         309
Score 123.5; Db ...
Pred. No. 2.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298
      Indels
                                                                                                                                                                                                    The receptor proteins
                            Length
                               309;
     73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rhodopsin;
                                                                                                                        pathology
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             204
     17;
```

Š

1 MLESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKM-APLDLLLSCLAVSRIFLQ 59

```
RESULT
W59924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
This polypeptide comprises HNFDY20, a novel human 7-transmembrane 6-protein coupled receptor that shows about 30.8% identity in 299 amino acid residues with the thrombin receptor. Its amino acid sequence with the thrombin receptor. Its amino acid sequence was deduced from an isolated HNFDY20 polynucleotide sequence (see V53631). The invention relates to HNFDY20 polypeptides and recombinant materials and methods for their
                                                                                                                                                  New polynucleotides and polypeptides encoding a novel human 7-transmembrane receptor - useful for diagnosing and treations cancer, osteoporosis and Parkinson's disease and infections
                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HNFDY20; G-protein coupled receptor; human; infection; HIV; pain, cancer; anorexia; asthma; Parkinson's disease; acute heart failu: hypotension; hypotension; urinary retention; osteoporosis; anyina pectoris; myocardial infarction; ulcer; allergy; benign prostatic hyportrophy; psychosis; anxiety; schizophrenia; manic depression; delirium; dementia; mental retardation; dyskinesia; Huntingdon's disease; Gilles de la Tourette's syndrometric dyskinesia; Huntingdon's disease; Gilles de la Tourette's syndrometric dyskinesia;
                                                                                                           Claim
                                                                                                                                       by HIV-1 or -2.
                                                                                                                                                                                                                                                           Bergsma
                                                                                                                                                                                                                                                                                                                     19-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                 16-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                             23-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ното
                                                                                                                                                                                                                                                                                       (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                          EP866126-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  therapy; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human 7-transmembrane receptor HNFDY20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W59924;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W59924 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263 -npviyiifnkqf----rncmlqlicc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                              1998-482962/42
DB; V53631.
                                                                                                                                                                                                                                                                                                                                                                                                                                    sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gidyytlkpevnne---sfviymfvvhftipliif-fcygglvftvkeaaaqqqes-att
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qkaekevtrmvilmviaflicwvpyasvafyifthqgsnfgpifmripaffaksaaiy--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVPGRGAPISALLSILSFLILYFSHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFIFYVNVIVIFFIEFIMCSANCAILLFINEL-----ELWLATWLGVFYCAKVASVR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mlaaym---fllivlgfpinfltlyvtv----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --KFFSQNATIQKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVAGS 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         genhaimgvaftwv-malacaappiagw-----sry----ipeglqcsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---HPL----FIWLKMRISKLVP----WMILGSLLYVSMICVFHSKYAGFMVPYFLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lggftstlytslhgyfvfgptgcnlegffatlggeialwslwlaieryvvvckpmsnfrf 110
                                                                                                                                                                                                                                                          Ŋ,
                                                                                                        Page
                                                                                                                                                                                                                                                           Fuetterer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first
                                                                                                         18-19;
                                                                                                                                                                                                                                                                                                                   97US-0820521
                                                                                                                                                                                                                                                                                                                                               98EP-0301122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                        24pp; English.
                                                                                                                                                                                                                                                          WS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401
                                                                                                                                                                                                                                                          Mao JY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        À
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
                                                                                                                                                                                                                                                          Sathe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -qhkklrtpinyillnlavadlfmv
                                                                                                                                                                                                                                                          8
                                                                                                                                                   and treating e.g. infections caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    failure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50
```

```
WATERSOLLE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 71; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, ulcers, allergies, benign prostatic hypertrophy, and psychotic and neurological disorders, including anxiety, schizophrenia, manic depression, delirium, dementia, severe mental retardation and dyskinesias, such as Huntingdon's disease or Gilles de la Tourette's syndrome. Gene therapy using RNA encoding HNFDY20 can be used to treat conditions caused by under-expression of the protein. The invention also relates to methods of identifying agonists and antagonists and for using such compounds to treat conditions associated with HNFDY20 imbalance. Diagnostic assays for detecting diseases associated with inappropriate HNFDY20 activity or levels are also provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production. It also provides methods for using such polypeptides and HNPDY20 polynucleotides for treatment of infections such as bacterial, fungal, protozoan and particularly HIV-1 or HIV-2 infections, and conditions including pain, cancers, anorexia, asthma, Parkinson's disease, acute heart failure, hypotension,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W37976;
                                                                                                                                                                                                                                                                                                                                                                                                             Kaposi's sarcoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR primer; KSHV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaposi's sarcoma associated herpesvirus G protein-coupled receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W37976 standard;
                                 Cesarman
                                                                                                                                                                                                                       09-OCT-1997;
                                                                                                                                                                                                                                                                                      16-APR-1998.
                                                                                         (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 angmhwplpfilcplsg--fiffttiyl-talflaavsierflsvahpl--wyktrprlg 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLLAVIQELLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLAI----QIESEVABESVPLLIFLFAVLLLIFSLGR---HTRQMRNTVAGSRVPGRGAP 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     I----FFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKMR---- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fsvylltflvglpln-llalvvfvgklqrrpva-vdvlllnltasdlllllflpfrmvea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vagllaatlInflvcfgpynvshvvgyicgespawriyvtllstlnscvdpfvyyf 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qlaillpvrlemavvlfvvpliitsycysrlvwilgrggshrrqrr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qaglvsvacwllasahcsvvyviefsgdishsq-----gtngtcylefrkd 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---ISKLVPWMILG---SLLYVSMIC--VFHSKYAGFMVPYFLRKFFSQNATIQ---KED 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISALL--SILSFLILY----FSH-----C-----MIKVFLSSLKFHIRRFIFLF 261
                                    H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                 Knowles DM;
                                                                                                                                                           96US-0728603.
                                                                                                                                                                                                                          97WO-US18216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORF74; Kaposi's sarcoma; diagnosis; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.1%; Score 122.5; DB 19; 24.0%; Pred: No. 4.3e-06; tive 53; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _ <u>- :- :-</u> :=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
                                                                                                                                                                                                                                                                                     W25926 W2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of a G-protein-coupled receptor encoded by ORF74 of Kaposi's sarcoma herpesvirus (KSHV). It can be used in the diagnosis and treatment of KHSV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated Kaposi's sarcoma-associated herpesvirus proteins comprising antigenic membrane protein, G protein coupled receptor and cyclin protein used to develop products for diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-261008/23
N-PSDB; V31718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 51-53; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allele; Xenopus laevis; melatonin; receptor; untranslated region; PCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signalling; inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W25926 standard; Protein; 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus melatonin receptor MEL-1Aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 mflfpniistglcrleiff----yylyvyldifsvvcvslvryllvaystrswpk---kq
Domain
                                                          Domain
                                                                                                                                                                         Domain
                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus
                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 LILYFSHCMIKVFLSSLKFHIRR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 ilsli-flinvlgnglvtyi----fckhrsragaidilllgiclnslclsisl--laevl 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 LLAVIQELLGIETNGIIVVVNGIDLIKHRKMA-PLDLLLSCLAVSRIELQLEIEYVNVIV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vllffvfcfpyhvlnlldtllrr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVAEFSVPLLIFLFAVLLLIFSLG----RHTR-QMRNTVAGSRVPGRGAPISALLSILSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     slgwvltsaallialvlsgdacrhrsrvvd---pvskqamcyenagnmtadwrlhvrtvs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVPWMILGSLLYVSMI-----CVFHSKYAGFMVPYFLRKFFSQNATIQKED-TLAIQIFS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFI-----WLKMRISK 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vtagfllpl-----allilfyaltwcvvrrtklqarrkvrg---
                                                                                                                                                                                                                                                                                                                                                                                                                                        Laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               342 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
      108.125
/note= "transmembrane domain 3"
                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                             'note-
                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                          /note=
                                                                                         'note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.9%; 5c.
22.4%; Pre
36;
                                                                                                                                                                                                                                                                  "transmembrane domain
                                                                                                                                                                                                                                                                                                                          "Extracellular N-terminal domain"
                                                                                   extracellular domain 2"
                                                                                                                                                "transmembrane
                                                                                                                                                                                                     "intracellular domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 120.5; DB Pred. No. 6e-06; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -vivav 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 215
```

14;

```
밁
                         õ
                                                   В
                                                                          Ş
                                                                                                   В
                                                                                                                      õ
                                                                                                                                                  Matches
                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                          receptor MEL-1A proteins. This sequence is a new form of the melatonin receptor designated MEL-1Aa, also known as Mel 1-c(alpha). The protein differs from previously known receptors by being 65 amino acids shorter and also having 2 different C-terminal amino acids. The protein is encoded by 2 different alleles (T79063-4) which differ in the 3'
                                                                                                                                                                                                                                  phosphodiesterase.
                                                                                                                                                                                                                                       untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The coding sequence was isolated from CDNA derived from Xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a 7 transmembrane receptor involved in cellular signalling. MEL-lAa has been shown to inhibit adenylyl cyclase, but both proteins can modulate intracellular CGMP, esp. inhibiting its accumulation induced by an inhibitor of
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Sequences W25926-7 represent novel allelic
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Page 25-26; 62pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
      139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-132635/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ADIR ) ADIR & CIE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9704094-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                     84
                                                                            61
                                                                                                    31
                                                                                                                           N
                     RISKLV----PWMILGSLLYVSMICVFHSKYAGFMV--PYFLRKFFSQNATIQKEDTLAI
                                            ypypviliaifqngwtlgnihcqisgflmglsv----igsvfnitaiainrycyichsl
                                                                    FIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKM
                                                                                                                    LESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPL-DLLLSCLAVSRIFLQL
rydklynqrstwcylgltwiltiiaivpnffvgslqydprifsctfaq--tvsssytitv 196
                                                                                             1 Similarity
57; Conserv
                                                                                                                                                                                                            354
                                                                                                                                               7.8%;
ilarity 19.4%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Marullo
                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95FR-0008947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-FR01167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
194..2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note=
172..19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "intracellular 152..171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . . 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "intracellular C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strosberg
                                                                                                                                                 64;
                                                                                                                                               Score 118; DB 18;
Pred. No. 1.2e-05;
4; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis melatonin
a new form of the melatonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ພູ
                                                                                                                                                                   Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain"
                                                                                                                                               Indels
                                                                                                                                               54;
                                                                                                                                            Gaps
                      174
                                               138
                                                                       120
                                                                                               83
                                                                                                                      60
                                                                                                                                             12;
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                               Jockers R,
                                                (ADIR ) ADIR & CIE.
                                                                                 24-JUL-1996;
                                                                                                 06-FEB-1997.
                                                                                                                WO9704094-A1
                                                                                                                                          Domain
                                                                                                                                                          Domain
                                                                                                                                                                                          Domain
                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                  Allele; Xenopus laevis; melatonin; receptor; untranslated region; pCR; mRNA; half-life; skin; amplification; primer; polymerase chain reaction; transmembrane domain; cellular signaling; inhibition; adenylyl cyclase; modulation; intracellular; cyclic GMP; inhibitor; phosphodiesterase.
                                                                                                                                                                          Domain
                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W25927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W25927 standard; Protein; 354
                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus melatonin receptor MEL-lAb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175
       1997-132635/12.
DB; T79065-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     waplnfiglavainpfhvapkipewlfvlsyfmayfnsclnaviygvlngnfrk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vvvhflvplsvvtfcyl-riwvlvlqvkhrvrqdfkqkltqtdlrnfltmfvvfvlfavc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQ--
                                                                                                                                                                                                                                                                                                                                                                                                     laevis
                               Marullo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GSRV---PGRGAP-ISALLSILSFLILYFSHCMIKVFLSSLKFHIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                95FR-0008947
                                                                                 96WO-FR01167
                                                                                                                                                                                                                                                                                                                                             /note=
57..68
                                                                                                                                                                                                                                                                                                                                                             /note-
33..56
                                                                                                                                                                                                                            194..219
                                                                                                                                                                                                                                            172..193
                                                                                                                                                                  /note-
                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                 note-
                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                    /note-
                                                                                                                                                                                                                                                                   note-
                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                    /note-
                                                                                                                                                                                                                                                                                                                                     /note-
                               s
                                                                                                                                                                                                                                                                                            .125
                                                                                                                                                                                                                                                                             . 151
                                                                                                                               "intracellular C-terminal domain"
                                                                                                                                                "transmembrane
                                                                                                                                                                "extracellular
                                                                                                                                                                                 "transmembrane
                                                                                                                                                                                                 "intracellular
                                                                                                                                                                                                                "transmembrane
                                                                                                                                                                                                                                                                                  "transmembrane
                                                                                                                                                                                                                                                                                                  "extracellular domain 2"
                                                                                                                                                                                                                                                                                                                   "transmembrane domain 2"
                                                                                                                                                                                                                                                                                                                                   "intracellular
                                                                                                                                                                                                                                 "extracellular
                                                                                                                                                                                                                                                  "transmembrane
                                                                                                                                                                                                                                                                   "intracellular
                                                                                                                                                                                                                                                                                                                                                   "transmembrane
                                                                                                                                                                                                                                                                                                                                                                    "Extracellular N-terminal domain"
                              Strosberg AD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3
                                                                                                                                                domain
                                                                                                                                                                                 domain
                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                  domain 3"
                                                                                                                                                                                                                                                                  domain 2"
                                                                                                                                                                domain
                                                                                                                                                                                                                 domain
                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                  domain 3"
                                                                                                                                                                                                                                                                                                                                                    domain 1"
                                                                                                                                                                                                                                                                                                                                   domain 1"
                                                                                                                                                                                                 ų
                                                                                                                                                                4
                                                                                                                                                                                 9
                                                                                                                                                                                                                 ធ្វ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -MRNTVA------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213
```

```
Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
FT FT M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       망
                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor designated MEL-IAb, also known as Mel 1-c(beta). The protein differs from previously known receptors by being 65 amino acids shorter and also differs throughout the sequence by 6 amino acids. The protein is encoded by 2 different alleles (T79065-6) which differ in the 3' untranslated region (both sequences encode the same protein), which is thought to affect the half-life of the mRNA. The coding sequence was isolated from cDNA derived from xenopus skin RNA and amplified using the primers T79067-76. The nucleotide sequence encodes a 7 transmembrane receptor involved in cellular signalling. MEL-IAb has been shown to modulate intracellular cGMP, esp. inhibiting its accumulation induced by an inhibitor of phosphodiesterase, but unlike the MEL-IAb protein, it cannot inhibitor daminimum and the metallic accumulation induced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding functional melatonin receptor of Xenopus for screening for potential (ant)agonists useful for e.g. treating cardiovascular disease and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequences W25926-7 represent novel allelic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor MEL-1A proteins. This sequence receptor designated MEL-1Ab, also known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cannot inhibit adenylyl cyclase activity.
                                                                                                                                 Melatonin receptor; G-protein-coupled receptor; glycosylation; disulfide bond; ligand binding pocket; phosphorylation; cytochrome-c family heme binding site; melatonin receptor-agonist; melatonin receptor-antagonist; circadian rhythm disorder; jet-lag; day-night cycle disorder; ovulation; reproductive cycle; antibody; animal breeding; puberty; transgenic animal; drug screening.
                                                                                                                                                                                                                                                          High-affinity melatonin receptor
                                                                                                                                                                                                                                                                                            15-AUG-1996
                                                                                                                                                                                                                                                                                                                                                             R88409 standard; Protein; 420
                                                                                                    Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                              256 waplnfiglavainplhvapkipewlfvlsyfmayfnsclnaviygllnqnfrk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139
                                                    Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31
                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPL-DLLLSCLAVSRIFLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GSRV---PGRGAP-ISALLSILSFLILYFSHCMIKVFLSSLKFHIRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RISKLY----PWMILGSLLYVSMICVFHSKYAGFMY--PYFLRKFFSQNATIQKEDTLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ypypviliaifqngwtlgnihcqisgflmglsv----igsvfnitaiainrycyichsl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vvvhfivplsvvtfcyl-riwvlviqvkhrvrqdfkqkltptdlrnfltmfvvfvlfavc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rydklfnqrstwfylgltwiltiiaivpnffvgslqydprifsctfaq--tvsssytitv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Page 30-31; 62pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,
                                  /note= "Extracellular domain"
                                                                  Location/Qualifiers
 /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7.8%;
                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                %; Score 118; DB 18;
%; Pred. No. 1.2e-05;
64; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis melatonin a new form of the melatonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -MRNTVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12;
```

```
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                        06-JUN-1995;
17-JUN-1994;
07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                             07-JUN-1995;
                                                                                                                                                                       Modified-site
                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                            Modified-site
                                                                                                      28-DEC-1995
                                                                                                                                WO9535320-A1
(MASS-) MASSACHUSETTS GEN HOSPITAL
                        95US-0319887.
94US-0261857.
94US-0319887.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
57..68
/note=
67..72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
33..57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Extracellular 105..182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94..107
                                                                              95WO-US07360
                                                                                                                                                                                                                                                                                                                                                                                                                258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-
                                                                                                                                                                                                 /note=
395
                                                                                                                                                                                                                                                  /note= "Protein-kinase-C phosphorylation 328
                                                                                                                                                                                                                                                                            /note=
320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Protein-kinase-C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132..137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125..131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108..126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                      302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Transmembrane region-V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194..220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note-
                                                                                                                                                                                                                                                                                                                                 296..300
                                                                                                                                                                                                                                                                                                                                                           280..301
                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Residue which may form ligand binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Intracellular loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "Residue which may form ligand binding pocket"
                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                  note=
                                                                                                                                                                                                                                                                                                                                                                                              note= "Residue which may form ligand binding pocket"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "Extracellular loop"
                                                                                                                                                                                    note-
                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                                                                        note= "Extracellular loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . . 151
                                                                                                                                                                                                                                                                                                        . 420
                                                                                                                                                                                                                                                                                                                                                                                                                                          259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Transmembrane region-III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Protein-kinase-C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Putative cytochrome-c family heme binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Transmembrane region-IV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Intracellular loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Region used to construct primer"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Conserved melatonin receptor motif"
                                                                                                                                                                                                                                                                                                                  "Conserved melatonin receptor-1b motif"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Transmembrane region-VI"
                                                                                                                                                                                    "Protein-kinase-C phosphorylation
                                                                                                                                                                                                              "Protein-kinase-C
                                                                                                                                                                                                                                       "Protein-kinase-C
                                                                                                                                                                                                                                                                                                                                          "Transmembrane region-VII"
                                                                                                                                                                                                                                                                                                                                                                                                                           "Region
                                                                                                                                                           "Protein-kinase-C
                                                                                                                                                                                                                                                                                          "Intracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                            used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               region-II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    loop"
                                                                                                                                                                                                                                                                                                                                                                                                                            construct primer
                                                                                                                                                                                                                                       phosphorylation
                                                                                                                                                            phosphorylation
                                                                                                                                                                                                            phosphorylation
                                                                                                                                                                                                               site"
                                                                                                                                                                                                                                        site*
                                                                                                                                                                                                                                                                  site"
                                                                                                                                                             site'
                                                                                                                                                                                      site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pocket"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site"
```

3333

Rattus

sp

```
RESULT W19105
ID W1
XX W1
XX W1
XX Z6
DT 26
DT 26
XX Ra
XX Ph
KW ma
KW ho
XX ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 57
                                                                Pheromone receptor; vomeronasal sensory neuron; social behaviour; maternal behaviour; reproductive behaviour; fertility;
                                                                                                                                                                                                         Rat pheromone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          form of a ligand binding pocket. Phosphorylation sites in the encoding bnA may be involved in receptor regulation. Primers from the encoding bnA may be used for isolation of sheep, mouse and human receptor sequences. Receptor fragments which interact with melatonin, or specific antibodies; may be used as receptor-agonists or receptor-antagonists. Agonists may be used in therapy of circadian rhythm disorders such as jet-lag or day-night cycle disorders, to control ovulation, or in alteration of reproductive cycles in seasonally breeding animals. Antagonists may be used to control the initiation or timing of puberty in humans. The receptor gene may also be expressed in a transgenic animal for use as a model system to screen agonists and antagonists.
                                          hormone
                                                                                                                                                                                                                                                                                      26-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                       W19105
                                                                                                                                                                                                                                                                                                                                                                                                                                                    W19105 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coupled to guanine nucleotide binding proteins (G-proteins), and has 7 hydrophobic putative transmembrane domains. The N-terminus has an N-linked glycosylation site typical for G-protein-coupled receptors, and 2 Cys residues in the lst 2 extracellular loops may form a stabilizing disulfide bond. Pro residues in transmembrane domains IV. V and VI may introduce kinks in the alpha-helices to form of a light of the lates and the lates to the lates are the lates to the lates are the lates and the lates to the lates are 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding high affinity melatonin receptor one - used to identify receptor agonists or antagonists e.g. for regulating circadian rhythm disorders or reproductive cycles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence 47,424) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5; Fig 1; 115pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             wap Infiglava in pfh vap kipewlfvlsyf may fn sclnaviy gvln qn fr kap for the school of the school 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rydklyngrstwcylgltwiltiiaivpnffvgslqydprifsctfag--tvsssytitv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RISKLV----PWMILGSLLYVSMICVFHSKYAGFMV--PYFLRKFFSQNATIQKEDTLAI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LESHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPL-DLLLSCLAVSRIFLQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vvvhfivplsvvtfcyl-riwvlviqvkhrvrqdfkqkltqtdlrnfltmfvvfvlfavc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQ-----MRNTVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ypypviliaifqngwtlgnihcqisgflmglsv----igsvfnitalainrycyichsl 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ltsalavvliftivvdvlg----nilvi---lsvlrnkklqnagnlfvvslsiadlvvav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1996-058368/06
DB; T09947.
                                          secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 19.4
57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GSRV---PGRGAP-ISALLSILSFLILYFSHCMIKVFLSSLKFHIRR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              420 AA;
                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                     receptor VN4
                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.8%; Score 118;
19.4%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     high-affinity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The receptor is a membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 17;
1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            melatonin receptor (mol.wt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
```

```
(W19103-09) are members of a novel family of presumed (W19103-09) are members of a novel family of presumed 7-transmembrane domain receptors that are evolutionary independent of the odorant receptors of the main olfactory epithelium (WOE). Their amino acid sequences were deduced from cDNA clones (see also T69545-50, VN2 sequence not provided) obtd. by differential cloning, PCR and hybridisation from single vomeronasal sensory neurons (VSN). Individual neurons express different complements of the receptors. VN polypeptides can be expressed in host-vector systems for use in identifying modulators for control of maternal, reproductive and social behavior, to increase fertility, control
                                                                                                                                                                  Nucleic acid molecule encoding vertebrate pheromone receptor - useful to identify modulators for control of reproductive and social behaviour, fertility and hormone secretion
 hormone secretion and to
                                                                                                                                              Disclosure; Page 79-80; 123pp; English.
                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                    Axel R,
                                                                                                                                                                                                                                                                                                                     18-OCT-1996;
                                                                                                                                                                                                                                                                                                                                           24-APR-1997
                                                                                                                                                                                                                                                                                                                                                                  W09714790-A1
                                                                                                                                                                                                                                                                                                                                                                                                                        Misc-difference 263..264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                         (UYCO ) UNIV COLUMBIA NEW YORK
                                                                                                                                                                                                                                                                                                19-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                        pheromone receptors VN1, VN3, VN4, VN5, VN6, VN7
                                                                                                                                                                                                                            1997-245107/22
                                                                                                                                                                                                                                                     Dulac
                                                                                                                                                                                                                                                                                                95US-0005698.
                                                                                                                                                                                                                                                                                                                     96WO-US16637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261
                                                                                                                                                                                                                                                                                                                                                                                                             /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 16..37
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "predicted VII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270..292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240..258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135..156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label- VII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "predicted V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194..212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "predicted III"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "predicted II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label- V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label=
                                                                                                                                                                                                                                                                                                                                                                                     "the amino acid sequence deduced from the nucleotide sequence has a lysine residue between Met-263 and Phe-264"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Ser-261 is additional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "predicted position of transmembrane \mathbf{I}"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٧
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ٧I
                                                                                                                                                                                                                                                                                                                                                                                                                                sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΙΙ
                                                                                                                                                                                                                                                                                                                                                                                                                                              residues
regulate food uptake
                                                                                                                                                                                                                                                                                                                                                                                                                                            deduced form the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             e
f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                            the amino acid
e nucleotide
                                                                                                                        and VN2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain
```

SXC

310

A,

Length 310;

animals Sequence

```
RESULT 12
W17836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                         Glucose transporter; GLUT-1; GLUT-2; chimeric transporter; diabetes; cancer; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                             W17836;
                                                                                                                                                                                                                                                                                                                                                                                                                                    W17836 standard; Protein; 522
                                                                                                                                                                                                                                                                                                                                                            Rat glucose transporter GLUT-2.
                                                                                                                                                                                                                                                                                                                                                                                    24-NOV-1997
                                                                                                                                                                                                                                                                             WO9715668-A2
                                                         Use of glucose transporter, GLUT-2 or GLUT-2 chimera(s) for cell-killing - used in negative and double selection protocols and screening methods, for cancer treatment and treatment of diabetes
                                                                                                                                                                                                                                                     01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135
This polypeptide comprises rat glucose transporter GLUT-2. A claimed chimeric transporter comprises a contiguous amino acid
                                    Claim 137; Page 115-119; 169pp; English
                                                                                                                     WPI; 1997-297737/27.
                                                                                                                                            Clark SA,
                                                                                                                                                                                                      23-OCT-1995;
                                                                                                                                                                                                                             23-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 20.8 nes 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIFYVNVIVIFFIEFIMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vreaffigl \verb|malssgy| lvaflwr hrk qaqhlhstglssksspeqratetill \verb|msffvvl| \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1---llcvlymcfsshli---lsiiatpnltsdnfmyvtkscsflpmcysrtsmfsttia 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYVSMICVFHSKYAGFMVPYFLRKFFSQNAT-----IQKEDTLAIQIFSFVAEFSVPLL 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stscqsliylhrlsrgftlsaacllnvfwmitlsskkscl----tkfkhnsphhisgaf 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SANCAILLFINELE----LWLATWLGVFYCAKVASVRHPLFIWLKMRISKLVPWMILGSL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yilenv--vfyssrmfkdgstfycvqiivshsyatvssfvfiftekrmtk----ilrsv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YFSHCMIKVFLSSLKFHIRRFIFLFFILVIGIYPSGHSLILILGNPKLKQNAKKFLLHSK 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               I---FLFAVL-----LLIFSLGRHTRQMRNT----VAGSRVPGRGAPISALLSILSFLIL 236
                                                                                                                                                                    BETAGENE INC.
UNIV TEXAS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306
                                                                                                                                           Newgard CB,
                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                      95US-0546934
                                                                                                                                                                                                                              96WO-US17327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.7%;
20.8%;
                                                                                                                                              Normington KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 117.5; DB 18; Pred. No. 1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                               Thigpen AE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
```

```
sequence from human GLUT-1 (see W17835) operatively linked to a contiguous amino acid sequence from rat GLUT-2. The GLUT-1/GLUT-2 chimeric transporter confers glucose sensing capacity to a cell without rendering the cell subject to diabetic immune destruction, and does not transport streptozotocin. The chimeric transporter may be expressed in vivo by administration of a claimed chimeric polynucleotide (see T66495-96) for treatment of diabetes, or expressed in a host cell to prepare a recombinant cell that secretes insulin in response to glucose and which can be administered to a patient to treat diabetes. GLUT-2 can also be used in claimed methods of cell killing, such as negative selection and double seletion protocols in vitro, in screening methods for identifying genes, promoters and substrates, and in cell killing in
                                                                                                                                               vivo, such as may be used in cancer treatment.
                                                                                               Sequence
                                                                                                  522
                                                                                                  ΑĄ,
7.7%; Score 117.5; DB 1
23.4%; Pred. No. 2.3e-05;
                             DB 18;
                          Length
```

```
Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                          302 ivvalmlhlaqqfsgi--ngifyystsifqtagis-----qpvyatigvgainmifta 352
435 alaafsnwycnfiialcfqyiadflgpyvfflfagvvlvftl 476
                                                                                                                     120 MRISKLVPWMILGSLLYVSMICVFHSKYAGFM-----VPYFL-RKFFSQNATIQKEDTL 172
                                                                                                                                                                   353
                                         173 AIQIFS-----FVAEFSVPLLIFLFAVLLLIFSL 201
                                                                                 385 lvlldkftwm-----syvsmtaif--lfvsffeigpgpipwfmvaeffsqg---prptal
                                                                                                                                                                                                  60 LFIFYVNVIVIFFIEFIMCSANCAILLFINELELWLATWLGVFYCAKVASVRHPLFIWLK 119
                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                6 LIIYFLLAVIQFLLGIFTNGI-----IVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQ 59
                                                                                                                                                             vsvllvek-----vfmslg
                                                                                                                                                                                                                                                                                                                          52;
                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                              35;
                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                62;
                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                73;
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                              434
                                                                                                                                                                         384
                                                                                                                                                                                                                                                                                                                                  11;
```

Q

Q 밁

В

RESULT 13 Y13352

Y13352 standard;

Protein;

690

25-JUN-1999

(first entry)

20 В Ş

23.4%;

망

```
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
17-SEP-1997;
                                                                           25-NOV-1997;
17-SEP-1997;
                                                                                                                                                                                                                                                             Secreted protein; transmembrane protein; human; enterocolitis; 2011nger-Ellison syndrome; gastrointestinal ulceration; congenital microvillus atroph; skin disease; cell growth; abnormal keratinocyte differentiation; psoriasis; epithelial cancer;
                                                                                                                                                                                                                                                                                                                           Amino acid sequence of protein PRO228
                                                                                                                                                                                                                                      parkinson's disease; Alzheimer's disease; ALS; neuropathy;
fibromodulin; dermal scarring; Usher Syndrome; Atrophia areata;
                                                                                                                    16-SEP-1998;
                                                                                                                                              25-MAR-1999
                                                                                                                                                                       WO9914328-A2
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                        anti-thrombotic;
97US-0059121.
97US-0059122.
97US-0059184.
                                      97US-0066840.
97US-0059113.
97US-0059115.
97US-0059117.
97US-0059119.
                                                                                                                    98WO-US19330.
                                                                                                                                                                                                                           wound healing;
                                                                                                                                                                                                                            tissue
                                                                                                                                                                                                                            repair.
```

```
CC Y13344-403 represent secreted and transmembrane human proteins.
CC The cNNA sequences are obtained from CDNA libraries, prepared from CC fetal lung, fetal kidney, fetal brain, fetal liver and fetal retina.
CC The encoded polypeptides have specific uses based on their homology to CC known polypeptides, e.g. PRO217 and PRO217 can be used for disorders CC associated with the preservation and maintenance of gastrointestinal CC uncosa and the repair of acute and chronic mucosal lesions (e.g. enterocolitis, Zollinger-Ellison syndrome, gastrointestinal CC ulceration and congenital microvillus atrophy), skin diseases associated with abnormal keratinocyte differentiation (e.g. psoriasis, epithelial CC concers such as lung squamous cell carcinoma of the vulva and gliomas), CC potent effects on cell growth and development, diseases related to growth CC or survival of nerve cells including Parkinson's disease, Alzhelmer's CC disease, ALS, neuropathies or cancer. PRO265 can be used as for CC fibromodulin, e.g. for reducing dermal scarring. PRO264 can be used as a target for anti-tumor drugs. PRO33 may be used in the treatment CC of Usher Syndrome or Atrophia areata; PRO269 can be used as an anti-thrombotic agent; PRO287 polypeptides and portions may have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1997;
21-NOV-1997;
24-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1997;
17-NOV-1997;
18-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                           Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-SEP-1997;
18-SEP-1997;
15-OCT-1997;
17-OCT-1997;
17-OCT-1997;
                                                                                                                                                                                                                                                               Claim 12; Fig 19; 320pp; English.
                                                                                                                                                                                                                                                                                          New isolated human genes and polypeptides used in, gastrointestinal ulceration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-NOV-1997
07-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-OCT-1997
31-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                   (GETH )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-OCT-1997
29-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-OCT-1997;
28-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 - OCT - 1997
27 - OCT - 1997
                                                                                                                                                                                                                                                                                                                                                                           Ġ
                                                                                                                                                                                                                                                                                                                                   1999-229533/19.
DB; X52222.
                                                                                                                                                                                                                                                                                                                                                                                                   GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                        Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0065186.
97US-0065846.
97US-0065693.
97US-0066120.
97US-0066364.
97US-0066772.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0063738
97US-0063734
97US-0064215
97US-0063735
97US-0063870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0059263.
97US-0059266.
97US-0062125.
97US-0062285.
97US-0062287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-0063704.
97US-0063732.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0063550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0063121.
                                                                                                                                                                                                                                                                                                                                                                       Gurney
                                                                                                                                                                                                                                                                                                                                                                       AL,
                                                                                                                                                                                                                                                                                                                                                                       Pennica D,
                                                                                                                                                                                                                                                                                                                                                                       Wood WI,
                                                                                                                                                                                                                                                                                                     e.g.
                                                                                                                                                                                                                                                                                                                                                                       Yuan
                                                                                                                                                                                                                                                                                                     treatment of
                                                                                                                                                                                                                                                                                                                                                                       ij
```

```
RESULT
Y83225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88888
8888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                      Modified-site
                                                                                            Modified-site
                                                                                                                                                                                                                                                                                   Inhibition; cancer; neoplasia; tumour; breast; ovary; renal; colorectal; uterus; prostate; lung; bladder; central nervous system; CNS; melanoma; leukaemia; pRO211; PRO228; PRO538; PRO172; PRO182;
Modified-site
                                              Modified-site
                                                                     Modified-site
                                                                                                                      Modified-site
                                                                                                                                            Modified-site
                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                   PRO288 Polypeptide
                                                                                                                                                                                                                                                                                                                                                              16-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                      Y83225
                                                                                                                                                                                                                                                                                                                                                                                                            Y83225 standard;
                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                             human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapeutic applications in wound healing and tissue repair; PRO317 can be used for treating problems of the kidney, uterus, endometrium, blood vessels, or related tissue, e.g. in the heart of genital tract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 611 enirscarga--lallfllgttwifgvlhvvhasvvtaylftvsnafq-gmfiflflcvl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     668 ---------srkiqeeyyrlfknvpcc 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 -GSRVPGRGAPISALLSILS----FLILYFSHCMI---KVFLSSLKFHIRRFIFLFFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 LFIWLKMRISKLVPWM-ILGSLLYVSMICVFHSKYAGFM-VPYFLRKFFSQNATIQKEDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            404 nhlthfailmssgpsigikdyniltritglgii-----isliclaic----iftf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIF 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVNVIVIFFIEF-----IMCSANCAILLFINELELWLATWLGVFYCAKVASVRHP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IGIYPSGHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lgyryygttkvcwlstennfiwsfigpacliilvnllafgvilykvfrhtaglkpevscf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAIQ------IFSFVAEFSVPLLIFLFAVLLLIFSLGRHTRQMRNTVA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ffl----aafawmciegihlylivvgviynk--gflhknfylfgylspavvvgfsaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w-----ffseiqstrttihknlccslflaelvfl----vgintntnklfcsiiagllhy
                                                                                                                                                                                                                                                                             88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                             (first
                                                                    /note=
52..58
                                                                                             /note= "|
4953..53
/note=
36..44
                      /note=
64..68
                                              /note=
54..58
                                                                                                                    /note=
50..56
                                                                                                                                            /note=
38..44
                                                                                                                                                                   /note=
21..25
                                                                                                                                                                                          /label Signal_peptide
15..19
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 690
                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.78;
          "N-glycosylation site"
                                                                                                                              "N-myristoylation
                                 "Casein kinase II phosphorylation site"
                                                       "N-myristoylation
                                                                                                      "N-myristoylation
                                                                                                                                                       "N-glycosylation site"
                                                                                                                                                                             "N-glycosylation
                                                                              "Glycosaminoglycan attachment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 117.5; DB :
Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                            ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298
                                                                                                                                                                             site"
                                                          site"
                                                                                                        site"
                                                                                                                                site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
```

```
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                   Modified-site
                                                                                                                                                                                     Modified-site
                                                                                                                                                                                                      Modified-site
                                                                                                                                                                                                                                      Modified-site
                                                                                                                  Modified-site
                                 Modified
                                                                                  Modified
Domain
                 Domain
                                                                 Domain
                                 l-site
                                                                                  -site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
68..72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= ."N-glycosylation site"
,35...139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
94..98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
80..86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=75..87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
74..78
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
76..80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Casein kinase II phosphorylation
127..131
                                                                                                                                                                                                                                                                7note= "0
                                                                                                                                                                                                                                                                                                                 /note= "1310..314
                                                                                                                                                                                                                       /note= "1
                                                                                                                                                                                                                                                                                                                                                                                    188..192
                                                                                                                                                                                                                                                                                                                                                                                                     181..185
                                                                                                                                                                                                                                                                                                                                                                                                                     177..181
                                                                                                                                                                                                                                                                                                                                                                                                                                     161..165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     150..154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note=
/label=
648..664
                                                                                                                                                                                                                                                                                                                                  249..253
                                                                                                                                                                                                                                                                                                                                                 244..248
                                                  /label=
573..593
                                                                   /note= "I
                                                                                                                                                                                                                                      381..385
                                                                                                                                                                                                                                                                                                                                                                                                                                            'note-
                 /note=
                                                                                                                                                                                     395..399
                                                                                                                                                                                                      388..394
                                                                                                                                                                                                                                                                                  346..350
                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                          'note=
                                                                                                                                                                                                                                                                                                                                                                                           note=
                                                                                                                                                                                                                                                                                                                                                                                                                             note=
                                                                                  /label= Transmembrane_domain 521..527
                                                                                                                                                                     430..450
                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                         note-
                                                                                                                                                                                                                                                                                                         'note=
                                                                                                                                                                                                                                                                                                                                         note-
                                                                                                                                                                                                                                                                                                                                                                   .90..194
                                                                                                                                                                                                                                                                                                                                                                                                            note=
                                                                                                                    480..486
                                                                                                                                   165..486
                                                                                                                                                    134..440
                                                                                                                                                                                              note-
                                                                                                                                                                                                              'note=
                                                                                                                                           'note=
                                                                                                                                                                             note-
                                          /label=
                                                                                                          note-
                                                                                                                                                            label= Transmembrane_domain
                                                                                                                          label- Transmembrane_domain
 . . 664
                 ..636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                         "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Tyrosine kinase phosphorylation
                                                                                                                                                                                                                                                                                                                                                                           "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                          "Casein kinase II phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                             "Casein
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Casein
                                                                                                                                                                                                                                                                                                                         "N-glycosylation
                                                                                                                                                                                                                                                                                                                                         "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                          "Casein kinase II phosphorylation
                                                                                                                                            "M-myristoylation site"
                                                                                                                                                                                                                              "N-glycosylation site"
                                                                                                                                                                                                                                                "CAMP and cGMP dependent phosphorylation site"
                                                                                                                                                                                                                                                                        "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                          "Casein kinase II phosphorylation
                                                                                                                                                                                                                                                                                                         "Casein kinase II phosphorylation
                                                                                                                                                                            "N-glycosylation site"
                                                                                                                                                                                                               "N-myristoylation
                                                                                                          "N-myristoylation site"
                                                                                                                                                                                              "N-myristoylation site"
                                                                         "N-myristoylation site"
                         "Casein kinase II phosphorylation
         Transmembrane_domain
                                           Transmembrane_domain
                                                         Transmembrane_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and Asp hydroxylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                             kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase II phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase II
                                                                                                                                                                                                                                                                                                                                                                                                                             I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                             phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                phosphorylation
                                                                                                                                                                                                               site"
                                                                                                                                                                                                                                                         protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site"
                                                                                                                                                                                                                                                                                                                                                                                                                              site"
                                                                                                                                                                                                                                                                                                                                                                                                                                              site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                site"
                                                                                                                                                                                                                                                                                                                                                            site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  site"
                                                                                                                                                                                                                                                                                           site"
                                                                                                                                                                                                                                                                                                           site"
                                                                                                                                                                                                                                                                                                                                             site"
                                                                                                                                                                                                                                                                           site"
                           site"
```

RESULT
P90554
ID P9
XX
AC P9
XX
AC P9
XX
DT 16
XX
DE BC

P90554 standard; protein;

349

B

15

Bovine rhodopsin

16-FEB-1990

(first

entry)

```
밁
                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                       망
                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                            Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                      Š
                                                                                       멍
                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query, Match
Best Local S
Matches 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition for inhibiting neoplastic cell growth and treating of ovary, uterus, prostate, lung and bladder, comprises PRO211, PRO538, PRO172 or PRO182 polypeptide or their agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200021996-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Compositions comprising a PRO211, PRO228, PRO538, PRO172 or PRO182 polypeptide or their agonists, mixed with a carrier is useful for inhibiting neoplastic growth and treating tumors such as cancers of breast, ovary, renal, colorectal, uterus, prostate, lung, bladder, central nervous system, melanoma and leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Figure 4; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yuan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashkenazi A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH
                                                                                                                                                                                                                                                                                                                                                                      450
                                                                                                                                                                                                                                                                            500
                                                                                                                                                                                                                                                                                                                                                                                                                                                               404
                                                                                                                                                                                   551
                                                                                                                                                                                                                                 172
                                                                                                                                                                                                                                                                                                                        114
  899
                                             266
                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 SHLIIYFLLAVIQFLLGIFTNGIIVVVNGIDLIKHRKMAPLDLLLSCLAVSRIFLQLFIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000-317943/27.
DB; Z93701.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          :|| : :| :| | : : : : : : | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : | | | | | : : : : | | : : | | | : : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | 
                                                                                                                                                                                                                                                                                                                     LFIWLKMRISKLVPWM-ILGSLLYVSMICVFHSKYAGFM-VPYFLRKFFSQNATIQKEDT
                                                                                                                                                                                                                                                                                                                                                                   YVNVIVIFFIEF-----IMCSANCAILLFINELELWLATWLGVFYCAKVASVRHP 113
                                                                                                                                                                                                                                                                            LAIQ---
                                                                                       enirscarga--lallfllgttwifgvlhvvhasvvtaylftvsnafq-gmfiflflcvl
                                                                                                                                -GSRVPGRGAPISALLSILS----FLILYFSHCMI----KVFLSSLKFHIRRFIFLFFILV
                                         IGIYPSGHSLILILGNPKLKQNAKKFLLHSKCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goddard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ĄĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0104080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-US23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Transmembrane_domain 670..677
/note= "Tyrosine kinase phosporter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC
-srkiqeeyyrlfknvpcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.7%;
                                                                                                                                                                                                           "Tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 117.5; I
Pred. No. 3.3e
59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΑL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein
         685
                                                  298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3e-05;
ses 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Napier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancers, pRO228,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΣI;
                                                                                                                                                                                                                                                                                                                                                                                  499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                        550
                                                                                                                                                                                                                                                                                                                                    171
                                                                                                     667
                                                                                                                                                 265
                                                                                                                                                                                            610
                                                                                                                                                                                                                                        213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
```

Bovidae.

Bovine rhodopsin; 5HT1c receptor.

```
밁
                                                                                                                                                                                                                                                                    ş
                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Line and the state of the state
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.6%; Score 116; DB 10; Length 349; Best Local Similarity 19.9%; Pred. No. 2.1e-05; Matches 63; Conservative 66; Mismatches 133; Indels 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence codes for bovine rhodopsin. See also P90549-P90554, P92111 and N90955.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 11; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding serotonin 5HTlc receptor - used for producing protein, antibodies and probes for studying receptor binding and screening drugs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1989-278308/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Axel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-1989;
167 OKEDTLAIQIFSFVAEFSVPLLIFLFAVLLLIFSLGRHTROMRNTVAGSRVPGRGAPISA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYCO-) COLUMBIA UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-SEP-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Domain
                                                                             153 aimgvaftwv-malacaap-plvgwsryipegmgc---scgidyytph--------
                                                                                                                                113 PL----FIWLKMRISKLVPWMILGSLLYV--SMICVFHSKYAGFMVPYFLRKFFSQNATI 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO8918149-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                               93 ttlytslhgyfvfgptgcnlegffatlggeialwslvvlaieryvvvckpmsnfrfgenh 152
                                                                                                                                                                                                                                                  65 VNVIVIFFIEFIMCSANCAILLFI----NELELW----LATWLGVFYCAKVASVR----H 112
                                                                                                                                                                                                                                                                                                           37 fsmlaaymfllimlgfpinfltlyvt----vqhkklrtplnyillnlavadlfmvfggft 92
                                                                                                                                                                                                                                                                                                                                               Jessell TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88US-0162654.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80800SD-OM68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "cytoplasmic loop."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290..310
/label= VII
/note= "transmembrane domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
38..62
/label= I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label V'note "transmembrane domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label IV
note "transmembrane domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= III
note= "transmembrane domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label II
note "transmembrane domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note- "transmembrane domain."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . . 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ..174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..133
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                   195
                                                                                                                                                                                                                                                                                                                                                                                                                             15;
```

밁 . 2

```
밁
                                 Ş
                                                                밁
                                                                                         δδ
                                                                                                                          B
313 qf----rncmvttlcc 324
                  283 KLKQNAKKFLLHSKCC 298
                                                256 iimvlaflicwlpyagvafyifthqgsdfgpifmtipaffaktsavy---npviyimmnk 312
                                                                                      227 LLSILSFLILYESHCMIKVFLSSLKFHIRRFIFL----FFILVIGIYPSGHSLILILGNP 282
                                                                                                                    196 eetnnesfviymfvvhfiipliviffcygglvftvkeaaaxqqqesattqkaekevtrmv
                                                                                                                  25,5
```

Search completed: March 15, 2001, 12:58:48 Job time: 1569 sec